

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 5, 2006, 11:36:04 ; Search time 32.6424 Seconds
(without alignments)
1630.025 Million cell updates/sec

Title: US-09-745-792A-11
Perfect score: 2947
Sequence: 1 MRAPGPALRPPLPLLLLL.....NETYLMQFMWGLYQVMEN 553

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	268.5	9.1	349	2 JC6311	interferon recepto
2	253.5	8.6	325	2 A47003	cytokine receptor
3	225	7.6	575	2 A49667	interleukin-10 rec
4	222.5	7.6	590	2 A45283	interferon alpha/b
5	199.5	6.8	560	2 S27387	interferon alpha r
6	198.5	6.7	489	2 A31555	interferon gamma r
7	198.5	6.7	578	2 I56215	interleukin-10 rec
8	198	6.7	557	2 A32694	interferon alpha/b
9	192.5	6.5	477	2 A34368	interferon gamma r
10	176.5	6.0	332	2 A49347	interferon gamma r
11	167	5.7	292	1 KFRB3	tissue factor prec
12	167	5.7	337	2 I38500	interferon gamma r
13	156	5.3	292	1 KFB03	tissue factor prec
14	156	5.3	295	1 KFH03	tissue factor prec
15	148.5	5.0	515	2 I39073	interferon alpha-b
16	147.5	5.0	917	2 I49699	glycoprotein i30 -
17	143	4.9	294	1 KPM53	tissue factor prec
18	142.5	4.8	896	2 I56563	interleukin-3 rece
19	131	4.4	896	1 A35782	cytokine receptor
20	128.5	4.4	1375	2 T13822	frizzled gene prot
21	128.5	4.4	1526	2 T13823	frizzled gene prot
22	127.5	4.3	3924	2 S37431	ankyrin 2, neuro
23	126.5	4.3	918	2 A36337	membrane glycoprot
24	125.5	4.3	2215	2 T00348	Lx11 protein - mou
25	125	4.2	537	2 B46535	interleukin 2 rece
26	124.5	4.2	2477	2 S14428	fibronectin precu
27	124	4.2	331	2 A54295	interferon alpha/b
28	124	4.2	331	2 S59501	interferon recepto
29	120.5	4.1	1651	2 T14160	transmembrane rece

30	120	4.1	918	2 A44257	interleukin-6 sign
31	118.5	4.0	26926	1 I38344	titin, cardiac mus
32	117.5	4.0	1222	2 C88504	protein B0361.3 [i
33	116	3.9	2029	1 TDFELK	protein-tyrosine-p
34	115.5	3.9	1612	2 T30805	dutti protein - mo
35	114.5	3.9	1912	2 A56178	protein-tyrosine-p
36	114	3.9	776	2 A46583	neuroendocrine-spe
37	114	3.9	878	1 A40091	interleukin-3 rece
38	114	3.9	2302	2 T14328	protein-tyrosine-p
39	114	3.9	2957	2 T33152	hypothetical prote
40	113	3.8	976	2 A36355	protein-tyrosine k
41	112	3.8	354	2 T24873	hypothetical prote
42	112	3.8	536	2 T27668	hypothetical prote
43	112	3.8	1162	2 S68438	leptin receptor, s
44	111.5	3.8	1128	2 A82939	membrane nuclease
45	110.5	3.7	658	2 S76909	hypothetical prote

ALIGNMENTS

RESULT 1

JC6311
interferon receptor-class II cytokine receptor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: JC6311
R:Gibbs, V.C.; Pennica, D.
Gene 186, 97-101, 1997
A:Title: CRF2-4: Isolation of cDNA clones encoding the human and mouse proteins.
A:Reference number: JC6311, MUID:97199375; PMID:9047351
A:Accession: JC6311
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-349 <GIB>
A:Cross-references: UNIPROT:Q8VHM7; UNIPARC:UPI000017C6DE; GB:U53696

Query Match 9.1%; Score 268.5; DB 2; Length 349;
Best Local Similarity 27.3%; Pred. No. 7.5e-12;
Matches 98; Conservative 53; Mismatches 157; Indels 51; Gaps 15;

QY	31	PCVSGGL	-----PKPANIITFLSINMKNVLQWTPPEGLQGVKVTYVQYFIYQG 78
DB	3	PCVAGWLGGLLPALGMIPPPPEKVMNSVFNILQWEP-APPKTNLIFTAQESYRS 61	
QY	79	KWLKSECRINIRTYCDLSAETSDEHYQYAKVIAWTKCKSWAESGFYPLETQIG 138	
DB	62	----FQDHCKRTASTQCDFS-HLSKY-GDYTVRVAELADEHSEWV-NVTFPCVEDTIIG 114	
QY	139	PPEVALTTDEKSISSVLTAPKWKRNPEDLPSVSMQIYSLKYNVSLNTKSNRTWSQCV 198	
DB	115	PPEMQIESLABSLRLFSAPQ-IENEPETW--TLKNIYDSWAYRVQYWKNGTNEKFQVS 171	
QY	199	TNHTLVLTWLEPNTLYCVHVESFVPGPPRRAQPSKOCARTLKQSEFEKAKIFWVLP 258	
DB	172	PDSEVRLNLEPWTTCIQVQGLLDQNTGESEFICERTGND---EITPSMIVAILI 228	
QY	259	ISITVLFVSVMGSIYRIYHVGEKH-----PANLILYGNFEFDKRF----FVPAEK 306	
DB	229	VSVLVVFLFLGCFVVLWLIYKTKTFTSRSGTSLPQHLKEFLGHPHHSTFLLSFPFPEE 288	
QY	307	IVINFTITLNI-----SDSKISHQDMSLLGKSSDVS-----SLNDPQPSGNLRPQRESEV 357	
DB	289	AEV-FDKLSIISESESGKQSPEDNCASEPPSPDGPPELESKDEAPS---PPHDDPKL 342	

RESULT 2

A47003
cytokine receptor family class II protein CRF2-4 precursor - human
C:Species: Homo sapiens (man)
C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C:Accession: A47003; G01418
R:Butfalla, G.; Gardiner, K.; Uze, G.

Genomics 16, 366-373, 1993
A;Title: A new member of the cytokine receptor gene family maps on chromosome 21 at less
A;Reference number: A47003; MUID:93300510; PMID:8314576
A;Accession: A47003
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-325 <LUT>
A;Cross-references: UNIPROT:Q08334; UNIPARC:UPI0000048F14; GB:Z17227; NID:g3933378; PIDN:
R;Lutfalla, G.
submitted to the EMBL Data Library, April 1994
A;Reference number: G06935
A;Accession: G01418
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-123,'D',125-268,'VGRME' <LU2>
A;Cross-references: UNIPARC:UPI000016A09D; EMBL:U08988; NID:g571295; PID:g571296
C;Genetics:
A;Gene: GDB:CRFB4; CRF2-4
A;Cross-references: GDB:138168; OMIM:123889
A;Map position: 21q; 21q22.1-21q22.2
A;Introns: 17/1; 58/2; 111/1; 166/3; 216/1
C;Keywords: transmembrane protein

Query Match 8.6%; Score 253.5; DB 2; Length 325;
Best Local Similarity 25.1%; Pred. No. 8.2e-11;
Matches 84; Conservative 58; Mismatches 141; Indels 51; Gaps 12;

QY 35 GGLPKPANITFLSINMKVQLWTPPEGLQGVKVTYVQYFIYQKKWLKNSCRNINRTY 94
Db 19 GMVPPENVRMNSVNFKNILQWSEFAFG-NLTFQAQVLSYR-----IFQDKMNTLTLE 73

QY 95 CDLSAETSDEYHQYAKVAKIWMCTKSKWAESGRFYFLETOIGPPEVALTTDEKSIISVV 154
Db 74 CDFSSLSKYGDHT--LRVRAEFADEHSDWNI-TFCEVDVTIIGPGMQVEVLADSLHR 130

QY 155 LTAP-----EKWKRNPEDLPVSMQOIYSNLKYNVLNKTNSRWTWSQCVTNHTLVLTWL 208
Db 131 FLAPKIKENEYETV-----TMKNVNSWTYNQVWKNGTDEKFIQTPQYDFEVLRLN 181

QY 209 EPNLTLCVHVSEFVPGPPRAQSEKQARTLKQSSSEFKAKIIFWVY---LPISITVFL 265
Db 182 EPWTTYCVQVGRPLDPRNKAGESEFVCEQTHDET-----VPSMWAVILMASVFMVC 235

QY 266 FSVMG-----YSYRVIHVCKEKKHPANLILYGNFDFKRFVPAEKIVINFIINIS 317
Db 236 LALLGCFSLWCYKTKYAFSPRNSLPQHL-----KEFLGHPHNTLLFPFSPFLS 286

QY 318 DLSKISHQDMSLLGKSSDVSLNDPQSGNLRPP 351
Db 287 DENDV-FDKLSVIAEDSE-SGKQNPQDSCSLGTP 318

RESULT 3
A49667
interleukin-10 receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: A49667
R;Ho, A.S.; Liu, Y.; Khan, T.A.; Hsu, D.H.; Bazan, J.F.; Moore, K.W.
Proc. Natl. Acad. Sci. U.S.A. 90, 11267-11271, 1993
A;Title: A receptor for interleukin 10 is related to interferon receptors.
A;Reference number: A49667; MUID:94068585; PMID:8248239
A;Accession: A49667
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-575 <RES>
A;Cross-references: UNIPROT:Q61727; UNIPARC:UPI0000023997; GB:L12120; NID:g437615; PIDN:
C;Genetics:
A;Gene: IL10R
A;Superfamily: interleukin-10 receptor IL10R
C;Keywords: cytokine receptor

Query Match 7.6%; Score 225; DB 2; Length 575;

Best Local Similarity 22.0%; Pred. No. 2.2e-08;
Matches 127; Conservative 79; Mismatches 224; Indels 148; Gaps 26;

QY 37 LPKPANITFLSINMKVQLWTPPEGLQGVKVTYVQYFIYQKKWLKNSCRNINRTYCD 96
Db 26 LPSPSYWFPEARFQHILHWKPIPN-QSESTYVEVALKQYGNSTWNDIHCRAQAALSCD 84

QY 97 LSAETSDEYHQ---YVAKVKAIMGTKSKWAESGRFYFLETOIGPPEVALTTDEKSIISV 153
Db 85 LTTFTLTLVHRSYGYRVARVAVNSQVSNWTTI-----ETRFTVDEVILTVD---SV 133

QY 154 VLTA-----PEKWRNPEDLPV--SMQOIYSNLK-YNVSVLNTKSNRTWTSQCVTN 200
Db 134 TLKAMDGIITGTHPPR----PTITPAGDEYEQFKDLRVYKISIRKFSSELKNATKRVKQ 189

QY 201 HTLVLTLPEPNTLYCVHVSEFVPGPPRAQSPSKQARTLKQSSSEFKAKIIFWVYLPIS 260
Db 190 EFTFTLVPIGVKFKCVKVJPRLESRLNKAEWSEQCCLITTEQ-----YFTVTNLSILVIS 245

QY 261 ITVFLFSVMGYSIYRIYHVCKEKKHPANL--ILYGNFDFKRFVPAEKI-----VINFI 312
Db 246 MLLFCGILVCLVLQWYI-----RHPGKLTPLVFKKPHD---FFPANPLCPETPDALHIV 297

QY 313 TLNISDDSKISHQDMSLLGKSSDVSLNDPQSGNLRPPQEEBEVVKHLGVASHL----- 366
Db 298 DLEVFPKVSLELRD-SVLHGSTD-----SGFGSGKPSLQTEESQFLLPGSHPQIQGTL 349

QY 367 -----MEIFCDSEBENTGTSFTQOESLSRITPPD-KTVIEYEV-----DVR----- 406
Db 350 GKEESPGLQATCG--DNTDSGICLQEPGLHSSMGPAWKQOLGYTHQDDSDVNLVQNSP 407

QY 407 -----TTDICA-----GPEQELSLQBEVSTQGTLLSQAALAVLGPOTLOYSYT 451
Db 408 GQPKYTQDASALGHVCLLEPKAPEKD---QVMVTFGYQKQTRWKAAGAAGPAECLDEEI 464

QY 452 PQQLDLPLAQBHHTOSEBGEPEEPSTTLVDMDPQTGLRCLCIPSLSS--FQDSEGCSPSEG 509
Db 465 PLTDAPDPELGVHLQDD-----LAWPP-----PALAAGYLKQESQGMASA-- 504

QY 510 DGLGEBGLLSRLYEPPADPRPGENETYLQMPMEWGL 547
Db 505 -----PPGTPSRQWNLTEWWSL 522

RESULT 4
A45283
interferon alpha/beta receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A45283; I48423; I48425; I48426; I48427; I48428; I48429
R;Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992
A;Title: Behavior of a cloned murine interferon alpha/beta receptor expressed in homospes
A;Reference number: A45283; MUID:92262522; PMID:1533935
A;Accession: A45283
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-590 <UZE>
A;Cross-references: UNIPROT:P33896; UNIPARC:UPI0000027A2F; GB:M89641; NID:g194111; PIDN:
R;Lutfalla, G.; Uze, G.
Gene 148, 343-346, 1994
A;Title: Structure of the murine interferon alpha/beta receptor-encoding gene: high-freq
A;Reference number: I48423; MUID:95047447; PMID:7958966
A;Accession: I48423
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 118-125 <RES>
A;Cross-references: UNIPARC:UPI0000000524; EMBL:U06237; NID:g497103; PIDN:AAA65003.1; PI
A;Accession: I48424
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 127-224 <RE2>

[illegible]

Db 495 FIILNTDTVAEVKHAEED-----LRKYSSQT-----SQDSGNYNNEEBESVGT 539

Qy 515 EGLSLRLYEPE-----APDRPPE-----NSTYL 538

Db 540 ESGQAVLSKAPCGGPGCVSPSPGTLEDGTCFLGNEKYL 577

RESULT 5

S27387

interferon alpha receptor type 1 precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S27387; S33770

R:Mouchel-Vieilh, B.; Lutfalla, G.; Mogensen, K.E.; Uze, G.

FEBS Lett. 313, 255-259, 1992

A:Title: Specific antiviral activities of the human alpha interferons are determined at t

A:Reference number: S27387; MUID:93076908; PMID:1446745

A:Accession: S27387

A>Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-560 <MOU>

A:Cross-references: UNIPROT:Q04790; UNIPARC:UPI000012D698; EMBL:X68443; NID:g431; PIDN:CA

A:Experimental source: MDBK cells

R:Ljm, J.K.; Langer, J.A.

Biochim. Biophys. Acta 1173, 314-319, 1993

A:Title: Cloning and characterization of a bovine alpha interferon receptor.

A:Reference number: S33770; MUID:93305725; PMID:8318540

A:Accession: S33770

A>Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-421, 'V', 423-560 <LJM>

A:Cross-references: UNIPARC:UPI0000167C2D; EMBL:L06320; NID:g163187; PIDN:AAA02571.1; PII

A:Experimental source: lung

C:Keywords: antiviral; cytokine receptor; transmembrane protein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-560/Product: interferon alpha receptor type 1 #status predicted <MAT>

Query Match 6.8%; Score 199.5; DB 2; Length 560;

Best Local Similarity 29.1%; Pred. No. 1.5e-06;

Matches 60; Conservative 40; Mismatches 91; Indels 15; Gaps 9;

Qy 19 LLLLAAPWGRAVPCVSGGLP-KPANITFLSNMKVNLQWTPPEGLOGVK-VVTVQYFIY 76

Db 10 LMLVAGRW--VLPAASGANLKPENVEIHIIDDNFLKWN--SSSESVKNVTFSDYQIL 65

Qy 77 GQKWLKNSKCRNINRTYCDLSA-ETSDYHQYAKVKAIMGTKCSKMAESGRFYPFLET 135

Db 66 GTDNWKKLSGCOHITSYKCNFSSVELENVFEKIELRIRAEENNTSTWVEVPFVPLEA 125

Qy 136 QIGPEVALTTDEKISIVVLTAPEKWKKNPBDLPVSMQOIYSNLKYNVSV-LNTKSNRTW 194

Db 126 QIGPDPVHLEAEKRAIILSIPP---GKDSIMWAMDR--SSFRYSVVIWKNSSSLEER 179

Qy 195 SQCVNTHLVLTWLEPNTLYCVHVES 220

Db 180 TETVYPEDKIYK-LSPEITYCLKVKA 204

RESULT 6

A31555

interferon gamma receptor precursor - human

C:Species: Homo sapiens (man)

C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004

C:Accession: A31555

R:Aguet, M.; Dembic, Z.; Merlin, G.

Cell 55, 273-280, 1988

A:Title: Molecular cloning and expression of the human interferon-gamma receptor.

A:Reference number: A31555; MUID:89003065; PMID:2971451

A:Accession: A31555

A:Molecule type: mRNA

A:Residues: 1-489 <AGU>

A:Cross-references: UNIPROT:P15260; UNIPARC:UPI000002CE40; GB:J03143; NID:g184650; PIDN:f

A:Genetics:

A;Gene: GDB:IFNGR1; IFNGR
A;Cross-references: GDB:120688; OMIM:107470
A;Map position: 6q23-6q24
C;Superfamily: interferon gamma receptor
C;Keywords: cytokine receptor; transmembrane protein

Query Match 6.7%; Score 198.5; DB 2; Length 489;
Best Local Similarity 21.6%; Pred. No. 1.9e-06;
Matches 104; Conservative 76; Mismatches 199; Indels 101; Gaps 22;

QY 37 LKPNATITLSINMKVNLQ-----TPPEGLQGVKVTYVQYFYIGK--KWLKNSC 87
DB VPTPTNTVITSYNNNDIVYWEYQIMQVP-----VFTVEVKNYGVKNSWID--AC 77
QY 88 RNINRYCDLSARTSDYEQYAKVKAJWGTCCKWAESGRFPFLETOIGPEVALITD 147
DB INISHHYCNISDHVGDPNSLWVRKARVGQKESAYAKSEFAVCRDGIKPPKLDIRKE 137
QY 148 EKSIISVLTAPKWKRNPD-----LPVSMQOIY-----SNLYNVSVLNTKSNRT 193
DB 138 EKQIMIDIFHPSVFVNGDQEVYDYPETTCYIRVNVYVMNGSEIQYKI-LTKEDDCD 196
QY 194 WSCVTNHTLVLTWLEPNTLYCVHVESFVPPRRAPQSEKQCARLYKDQSEFFKAKIIP 253
DB 197 EIQC-----QLAIPVSSLNSQYCVSAGVLHVWGVTTEKSEKVCITIF--NSIKGSL-- 247
QY 254 WYVLPISITVFLFSVMG--YSIYRYIHVGKEKHPANLILYGNFEFKRFFVPAEKI-VINP 311
DB 248 W--IPVVAALLFLVLUSLVFCPIY---KKINPLK-----EKSIILPKSLISVRS 293
QY 312 ITLINISDDSK-----ISHQDMSLGG-----SSDVSSLNDPQPSGNLRPPQE----- 353
DB 294 AILETKPEKSYVSLITSYQPSLEKEVCEEPPLSPATVPGMHTDNPQKVEHTEELSSIT 353
QY 354 -----EEVKHGLGYASHLMEIFCDSENTGTSFTQOE--SLSRITPPDKTVIEYDYVR 406
DB 354 EVVTTENIPDVVPGSHLTPI---ERESSPLSSNQSEPGSIALNSYHSRNCSESDHSRN 410
QY 407 TTDICAGPEQEQLSQE-----EVSTQGLLESQAALAVLGPQTILQYSTPQLQDL 457
DB 411 GFDTSSCLSHSSUSDSDFPPNKKGEIKTEG----QELITVIKAPTSGYDKPHVLVDL 466

RESULT 7
I56215
interleukin-10 receptor - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I56215
R;Liu, Y.; Wei, S.H.; Ho, A.S.; de Waal Malefyt, R.; Moore, K.W.
J. Immunol. 152, 1821-1829, 1994
A;Title: Expression cloning and characterization of a human IL-10 receptor.
A;Reference number: I56215; MUID:94165477; PMID:8120391
A;Status: preliminary;
A;Molecule type: mRNA
A;Residues: 1-578 <RES>
A;Cross-references: UNIPROT:Q13651; UNIPARC:UPI00000012BB; EMBL:U00672; NID:9482802; PID
C;Genetics:
A;Gene: GDB:IL10R; HIL-10R
A;Cross-references: GDB:330958; OMIM:146933
A;Map position: 11q23.3-11q23.3
C;Superfamily: interleukin-10 receptor IL10R
C;Keywords: cytokine receptor

Query Match 6.7%; Score 198.5; DB 2; Length 578;
Best Local Similarity 21.6%; Pred. No. 1.9e-06;
Matches 130; Conservative 85; Mismatches 238; Indels 149; Gaps 29;

QY 16 PLLLLLLLAAPGRAWPCVSGG--LPKPNATITLSINMKVNLQWTPPEGLQGVKVTYVQY 73
DB 3 PCLVLLAALLSLRLGSDAHGTLPSPSPVWFEEAFHHILHTWTPIN-QSESTCYEVAL 61

QY 74 FYGQKKWLKNGEGRNINRYCDLSAETSDEYHQ--YYAKVKAJWGTCCKWAESGRFPY 131
DB 62 LRYGIESWNSISNCQ--TLSY-DLTAVTLLDLYHNGYRARVRAVDGSRHSNWTVT----- 114
QY 132 FLETOIGPPEVALTTDEKSI-----SVVLTAPKWKRNPDLPVSMQOIYSLNK-Y 181
DB 115 --NTRFSDVDEVTLTGVSVNLEIHNGFILGKIQLPRPKMAPAND-----TVESIFSHFREY 167
QY 182 NVSVLNTKSNRTWSQCVTNHT--LVLTWLEPNTLYCVHVESFVPPRRAPQSEKOCART 239
DB 168 EIAIRKVPQGNFTFTHKVKHENFSLTSGEVGE-FCVQVKPSVASRSNKGMSKEBCISL 226
QY 240 LKQSESEFKAKIIFWVLPISITVFLFSVMGYSIYRYIHVGKE-----KHPANLIL 290
DB 227 TRQYFTVTVNVIFFAFVLLLS-----GALACLALQLYVRRKKLPVLLFKKPSFFIF 280
QY 291 IYG-----NEFDKRFVPAEKIVINFTLINISDDSKISHQDMSLLGKSSDVSSLN 340
DB 281 ISORPSPETQDTIHPLEDEAFLLKVSPELKN-LDLHGSTDGFGSTKPSLQTEEPQF-LLP 338
QY 341 DPQPS-----GNLRPPQEBEEVKHGLGYASHLMEIFCD--SEENTGTSFTQESLSRTIP 393
DB 339 DPHQADRTLNGEPP-----VLGDCSSGSSNSTSDSGICLQEPSLSPSTG 384
QY 394 PDKTVIEYDYVRTTDICAGPEQEQLSQEVEVSTQGLLESQAALAVLGPQTILQYSTPQ 453
DB 385 P-----TWEQOVGSNS--RGQDDSGIDLQV--NSEGRAGDTQ-----GGSALGHHSPP 429
QY 454 LQ---DLDPDA---QEHTDSBEGPBEPTTLVDWDPPQTRGLCIPSLSFDDQDSECEPS 507
DB 430 PEVPGPEEDPAVAFQGLRQTRCABEKATKT-----GCLLEE 465
QY 508 EG---DGLGEEGLSLRYEPPADRPDPGENETVLMQF-----MEEW 545
DB 466 ERLPDITGLGPK--FGCLVDEAGLHPALAKGYLKQDPLEMTLIASSGAPTQGNQPTTEW 523
QY 546 GL 547
DB 524 SL 525

RESULT 8
A32694
interferon alpha/beta receptor precursor - human
C;Species: Homo sapiens (man)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
C;Accession: A32694; S17112
R;Uze, G.; Lutfalla, G.; Gresser, I.
Cell 60, 225-234, 1990
A;Title: Genetic transfer of a functional human interferon alpha receptor into mouse cells.
A;Reference number: A32694; MUID:90124632; PMID:2153461
A;Accession: A32694
A;Molecule type: mRNA
A;Residues: 1-557 <UZE>
A;Cross-references: UNIPROT:PI7181; UNIPARC:UPI000002D51B; GB:J03171; NID:gl84645; PIDN:7
R;Lutfalla, G.
submitted to the EMBL Data Library, July 1991
A;Description: The structure of the human interferon alpha/beta receptor gene.
A;Reference number: S17112
A;Accession: S17112
A;Molecule type: DNA
A;Residues: 1-16, 'A', 18-329, 'V', 343-557 <LUT>
A;Cross-references: UNIPARC:UPI0000179801; EMBL:X60459; NID:g32671
C;Genetics:
A;Gene: GDB:IFNAR1; IFNAR; IPRC
A;Cross-references: GDB:120078; OMIM:107450
A;Map position: 21q22.1-21q22.1
A;Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3
C;Keywords: cytokine receptor; glycoprotein; transmembrane protein
F;1-2/Domain: transmembrane #status predicted <TRN1>
F;437-455/Domain: transmembrane #status predicted <TRN2>
F;50, 58, 81, 88, 110, 172, 254, 313, 314, 376, 416, 433, 507, 518, 537/Binding site: carbohydrate (Asn

[illegible]

A;Reference number: A34508; MUID:9009370; PMID:2532365
A;Accession: A34508
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-94, 'E', '96'-477
A;Cross-references: UNIPARC:UPI00000217CE; GB:M28223; NID:g194131; PIDN:AAA37898.1; PID:
R;Munro, S.; Maniatis, T.
Proc. Natl. Acad. Sci. U.S.A. 86, 9248-9252, 1989
A;Title: Expression cloning of the murine interferon gamma receptor cDNA.
A;Reference number: A36224; MUID:90083245; PMID:2531896
A;Accession: A36224
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 10-477 <MUN>
A;Cross-references: UNIPARC:UPI000016CE19; GB:M28995; NID:g194123; PIDN:AAA37895.1; PID:
R;Raval, P.; Obici, S.; Russell, S.W.; Murphy, W.J.
Gene 154, 219-223, 1995
A;Title: Characterization of the 5' flanking region and gene encoding the mouse interferon
gamma receptor
A;Reference number: I48941; MUID:95197006; PMID:7890167
A;Accession: I48941
A;Status: translation not shown; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-28 <RES>
A;Cross-references: UNIPARC:UPI000016CAB7; EMBL:U05960; NID:g454092; PIDN:AAA80980.1; PI:
C;Superfamily: interferon gamma receptor
C;Keywords: cytokine receptor; transmembrane protein

```

Query Match      6.5%; Score 192.5; DB 2; Length 477;
Best Local Similarity 20.7%; Pred. No. 3.8e-06;
Matches 116; Conservative 71; Mismatches 191; Indels 183; Gaps 24;

Qy      3  AGRPALRPLUPPILLLLLAAPWGRAVPCVSGGL-----PKPANITFLSINMK 51
Db      6  AAGRMIL-----LVVLMSAKVG-----SGALTSTEDPEPPSPVPTNVLKSVNLN 52

Qy     52  NVLQWTPPEGLQGVKT--YTQYFYIGOKMLNKSECRNINRTYCOLSAETSDYEHQYY 109
Db      53  PVVCWE---YQMSQTPFTVQVKY-SGSWTD--SCTNISDHCCNIYQIMYPDVSAM 105

Qy     110  AKYKAIWTKCSKWAESGFYPPLETOIGPEVAL--TTDEKISVVLTAPEKWKRNPEDL 168
Db     106  ARVKAIVKQESDYARKSEFLMCKLGKGVGGPGGLEIRKKEEQSLVLFHPE-----V 157

Qy     169  PVSMMQ-----IYNLKNYVSVLNTKSNRTWSQCVTNHTLVLTWLEPN 211
Db     158  VVNGESQGMFGDGSCTYFTDYVYVYHNRSGBILTKHTVEKEC--NETLCELNI SVS 215

Qy     212  TL---YCVHVESVUPGPPRAQBPSEKQCATLKDQSEFPKAKIIFWVLPISITVFLFSV 268
Db     216  TLDRYCISYDGISSEFQVRTEKSKDQVCIPPFHDD-----RKDSIWILVVAPLVTFTVI 270

Qy     269  MGSYIYRYIHVGKEKHPANLILYIGNEFDKRPVPVPAEKI--VINFTILNISDDSKIS-- 323
Db     271  L---VFAYWTKK-----NSFRKRSIMLPKSLISVVVKSATLETKPESKYSLVT 315

Qy     324  -HDMSLLGKSDVSSLNDPQPSGNLRPFQEEBEVKHLGYASHLMEIFCDSEENTEGTSF 382
Db     316  PHQ-----PAVLESET-----VIC-----329

Qy     383  TQESLSRTPIPPDKTVIEYDVRTTDCMGPEQELSLQEEVSTOGTLLSQAALAVLG 442
Db     330  --EPLSTVTAPD-----SPEAAE---QEELSKETKALEAGGTSAMT 367

Qy     443  PQ-----TLOYSYTPQLQDLPLAQHTDSEBEGPEEPSTT 478
Db     368  PDSFPTQRRSFSLISSNQSGPCSLTAYHSRNGSDSLGVSSGSSISDLBSLPNNSETK 427

Qy     479  LVDWDPQTGRLCIPSLSSFDQ 499
Db     428  MAEHDPPPVKKA-PMASGYDK 447

```

RESULT 10

A49947
interferon gamma receptor beta subunit - mouse
N;Alternate names: IFN-gamma R beta chain; IFN-gamma R species-specific cofactor; type I
C;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A49947
R;Hemmi, S.; Bohni, R.; Stark, G.; Di Marco, F.; Aguet, M.
Cell 76, 803-810, 1994
A;Title: A novel member of the interferon receptor family complements functionality of
A;Reference number: A49947; MUID:94170381; PMID:8124717
A;Accession: A49947
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-332 <HEM>
A;Cross-references: UNIPROT:Q63953; UNIPARC:UPI000022068; GB:S69336; NID:G545841; PIDN:
A;Experimental source: early B-cell line Y16
A;Note: sequence extracted from NCBI backbone (NCBIN:145654, NCBIP:145656)
C;Keywords: cytokine receptor

Query Match 6.0%; Score 176.5; DB 2; Length 332;
Best Local Similarity 25.5%; Pred. No. 3.2e-05;
Matches 71; Conservative 43; Mismatches 129; Indels 35; Gaps 11;

QY 9 LRPLP--LPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTP-PEGLOGV 65
Db 1 MRPLWLPSSLCLGLGA--AASSPDSFSQLAAPLNPRHLVYNDQILTWEPSPSSNDPR 58

QY 66 KVTYTVQY-PIYQKKWLKSECRNINRYCDLS--AETSDYEHQY--YAKYKAIWGTK 120
Db 59 PVYQVEYFIDGSMHRLLEPNCTDITETKCDITGGRLKLFPHFPFTVLRVRAKRGNT 118

QY 121 SKWAGSRFPFLETOIGPEVALTTDEKSIISVLTAPKWKRNPEDLPVSMQOIYSNLK 180
Db 119 SKWVGLPEQHYENVTVGPKNISVTPGKSLVIHFSP-----VFHGAT 165

QY 181 YNVSVLNTKSNRTWSQCV-----TNHTLVLTWLEPNTLYCVHVESFVPGPPRAQP----S 232
Db 166 FOYLHVHWEKSETQEQVEGPFKSNISVGLNLPYRVYCLQTEAQLILNKKIRPHGLLS 225

QY 233 EKQCARTLKDOSSEFKAKIIFWVLPISITVFLFSVMG 270
Db 226 NVSCHETTANASARLOOVIL-----IFLGIFALLGLTG 259

RESULT 11
KFRB3
tissue factor precursor - rabbit
N;Alternate names: coagulation factor III
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JU0441; S23681
R;Andrews, B.S.; Rehemtulla, A.; Fowler, B.J.; Edgington, T.S.; Mackman, N.
Gene 98, 265-269, 1991
A;Title: Conservation of tissue factor primary sequence among three mammalian species.
A;Reference number: JU0441; MUID:91200676; PMID:1840552
A;Accession: JU0441
A;Molecule type: mRNA
A;Residues: 1-292 <AND>
A;Cross-references: UNIPROT:P24055; UNIPARC:UPI0000136CA5; GB:M55390; NID:G165696; PIDN:
A;Experimental source: brain
R;Pawashe, A.; Ezekowitz, M.; Lin, T.C.; Horton, R.; Bach, R.; Konigsberg, W.
Thromb. Haemost. 66, 315-320, 1991
A;Title: Molecular cloning, characterization and expression of cDNA for rabbit brain tis
A;Reference number: S23681; MUID:92081032; PMID:1746002
A;Accession: S23681
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 33-292 <PAW>
A;Cross-references: UNIPARC:UPI000016C544; EMBL:X53521; NID:G1495; PIDN:CAA37597.1; PID:
C;Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
C;Superfamily: tissue factor
C;Keywords: blood coagulation; glycoprotein; lipoprotein; thiolprotein; thiolester bond; transmembrane

F;1-32/Domain: signal sequence #status predicted <SIG>
F;33-292/Domain: tissue factor #status predicted <MAT>
F;33-249/Domain: extracellular #status predicted <EXT>
F;250-271/Domain: transmembrane #status predicted <TM>
F;272-292/Domain: intracellular #status predicted <INT>
F;41,114,154,167,182/Binding site: carboxydrate (Asn) (covalent) #status predicted
F;79-87,216-239/Disulfide bonds: #status predicted
F;274/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match 5.7%; Score 167; DB 1; Length 292;
Best Local Similarity 22.5%; Pred. No. 0.00013;
Matches 70; Conservative 53; Mismatches 126; Indels 62; Gaps 13;

QY 10 RPPLPLPPLLLL--LAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPEGLOGVKV 67
Db 11 RGTAVPYTVLLGLLAAQVARADTTG-----RAYNLTKWSTNFKTILEWEP-----KSIDH 62

QY 68 TTYTVQYFIYGOKKWLKSECRNINRYCDLSAB-TSDYEHQYVYAKYKAIWGTKS----- 121
Db 63 VYTVQ--ISTRLENW--KSKCFLTAETECDLTDEVKDVGQTYMARVLSYPARGNNTGFP 119

QY 122 ---KWAESGRFPFLETOIGPEVALTTDEKSIISVLTAPKWKRNPEDLPVSMQOIYSN 178
Db 120 EBPFRNSPEFTPYLDNLGQPTI-----QSFEQVGTKLNVTVQDARTL 163

QY 179 LKYNVSVLNTKS-----NRT---W-----SQCVTNHTLVLTWLEPNTLYCVHVESFV 222
Db 164 VRNGTFLSRAVFGKDLNLYYWRASSTGKKTATNTNEFLIDVDKGENYCFVQAVI 223

QY 223 PGPPRAQSEKQOCARTLKDOSSEFKAKIIFWVLPISITVFLFSVMGYSIVRYIHV--- 279
Db 224 PSKRKRQRPESLITECTSREQ---RAREMFFIIGAVVVVALLIIVLSVTYVKCRKARAG 280

QY 280 --GKEKHPANL 288
Db 281 PSKGESSPLNI 291

RESULT 12
I38500
interferon gamma receptor accessory factor-1 precursor - human
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 09-Jul-2004
C;Accession: I38500; I38501
R;Soh, J.; Donnelly, R.J.; Kotenko, S.; Mariano, T.M.; Cook, J.R.; Wang, N.; Emanuel, S.I.
Cell 76, 793-802, 1994
A;Title: Identification and sequence of an accessory factor required for activation of t
A;Reference number: A49946; MUID:94170380; PMID:8124716
A;Accession: I38500
A;Molecule type: mRNA
A;Residues: 1-337 <RES>
A;Cross-references: UNIPROT:P38484; UNIPARC:UPI000012D65E; EMBL:U05875; NID:G463549; PIDN:
A;Experimental source: clone pSKI
A;Accession: I38501
A;Molecule type: mRNA
A;Residues: 1-63, 'Q', 65-337 <RE2>
A;Cross-references: UNIPARC:UPI00001514B0; EMBL:U05877; NID:G463551; PIDN:AA16956.1; PII
A;Experimental source: clone pJS3
C;Genetics:
A;Map position: 21
C;Keywords: cytokine receptor

Query Match 5.7%; Score 167; DB 2; Length 337;
Best Local Similarity 23.9%; Pred. No. 0.00016;
Matches 91; Conservative 49; Mismatches 161; Indels 80; Gaps 18;

QY 9 LRPLPLPPLLLL--LAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPEGLOGVK- 66
Db 1 MRPTLWLSLLLLGVFAAAAAPPDPLSQLPAPHPKIRLYNAEQLSWEPVALSNSTRP 60

QY 67 VYTVQYFIYGOKKWLKSECRNINRYCDLSAETSD-----ECRNINRYCDLSAETSD-----YEHQYVYAKYKAIW 116
Db 61 VVVRVQ--FKYTDSKNFTADIMSGVNCITATECDFTAAFPSAGFPDMFNVLRLRAEL 119

```
QY 117 GTCCKWAESGRYPFLETOIGPBE-VALTTDEKSIISVLTAP-----EK 160
Db 120 GALHSAAWVTWPFOHRYNNVTGPPENIEVTPGSGLIIRFSPFDIADTSTAFPCYVHY 179
QY 161 WKNRPEDLPVSMQIYSNLKYN-VSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVE 219
Db 180 WEKG-----GIQOVKGFPSNISLDNLKPSRVY--CLOVQAQLL-WNKSNIIFRVGHL- 229
QY 220 SFVPGPPRAQPSKQKARTLKQDSSEFKAKIIFWVLPISITVF-LFSVMGYSIYRYIH 278
Db 230 -----SNISCYETMADASTELQOVIL-----ISVGTFSLLSLVAGACE----- 267
QY 279 VGKEKHPANLILLYGNEFDKRFVPAEKIVINETILNISDDSKISHQDMSLLGKSSDVSS 338
Db 268 -----FLVLKRYGLIKWYFHTPPS-----IPLQIEBYLKDPTQPI-LEALDKDSSP 312
QY 339 LNDPQPSGNL--RPPQEEERV 357
Db 313 KDDVWDSVSIISPFKEQEDV 333

RESULT 13
KF903
tissue factor precursor - bovine
N;Alternate names: coagulation factor III
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JQ1319
R;Takayenoki, Y.; Muta, T.; Miyata, T.; Iwanaga, S.
Biochem. Biophys. Res. Commun. 181, 1145-1150, 1991
A;Title: cDNA and amino acid sequences of bovine tissue factor.
A;Reference number: JQ1319; MUID:92109720; PMID:1764065
A;Accession: JQ1319
A;Molecule type: mRNA
A;Residues: 1-292 <TAK>
A;Cross-references: UNIPROT:P10931; UNIPARC:UPI0000136CA3; GB:S74147; NID:G241438; PIDN:
A;Experimental source: adrenal gland
A;Note: part of this sequence, including the amino end of the mature protein, was confir
C;Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
C;Comment: Expression of tissue factor can be induced in a variety of tissues by certain
C;Superfamily: tissue factor
C;Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane
F;1-35/Domain: signal sequence #status predicted <SIG>
F;36-292/Product: tissue factor #status experimental <MAT>
F;36-248/Domain: extracellular #status predicted <EXT>
F;249-271/Domain: transmembrane #status predicted <TM>
F;272-292/Domain: intracellular #status predicted <INT>
F;43,153,181/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;81-89,215-238/Disulfide bonds: #status predicted
F;118,124/Binding site: carbohydrate (Thr) (covalent) #status predicted
F;274/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match 5.3%; Score 156; DB 1; Length 292;
Best Local Similarity 22.0%; Pred. No. 0.00082;
Matches 70; Conservative 50; Mismatches 118; Indels 80; Gaps 14;

QY 22 LAAPWGRAVPCVSGGLPKPA-----NITFLSINMKNVLTQTPP 59
Db 1 MATPNGRVPVCPQAAVARALLFGLVLIQAGVAGTTDVVVAYNITWKSINFKLTLEWEP- 59
QY 60 EGLQGVKVTYTVQYFYIGQKKLWLNKSECRNINITYCDLSAE-TSDYEHQYAKVKAIMG 118
Db 60 ---KPINHVYTVQ-ISPRLGNWKNK--CPVTNTCEDVTDIIVKNVRETYLARVLSYPAD 113
QY 119 KCSKWAEE-----SGRYPFLETOIGPBEVALTTDEKSIISVLTAPKWKKNRPEDLPVSMQ 173
Db 114 TSSSTVEPPFTNSPFTPYLETNLGQFTI-----QSFQGVGKLVNTVQ 157
QY 174 QIYSNLKYNVSVLNTKS-----NRT-----W-----SOCVTNHTLVLTWLEPNTLYCVH 217
Db 158 DARTLVANSAFSLSDVDVGKDLNLTLYWYKASSTGKATNTNGFLDIDVKGNYCFH 217
```

```
QY 218 VSEFVPG--PPRAQPSKQKARTLKQDSSEFKAKIIFWVLPISITVFLF-SVMGYSIY 274
Db 218 VQAVILSRNRNQKSPSPKICTSHEKVLSTE-----LFFIIGTVMVLIIIFIVLSVSLH 272
QY 275 RYIHV-----GREKHPAN 287
Db 273 KCKKRAERSGKENTPLN 290

RESULT 14
KFH03
tissue factor precursor [validated] - human
N;Alternate names: coagulation factor III
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A43645; A47574; A28320; A29062; A29672; A29008
R;Mackman, N.; Morrissey, J.H.; Fowler, B.; Edgington, T.S.
Biochemistry 28, 1755-1762, 1989
A;Title: Complete sequence of the human tissue factor gene, a highly regulated cellular
A;Reference number: A43645; MUID:89247359; PMID:2719931
A;Accession: A43645
A;Molecule type: DNA
A;Residues: 1-295 <MAC>
A;Cross-references: UNIPROT:P13726; UNIPARC:UPI000002CD0D; GB:J02846; NID:G339505; PIDN:
R;Fisher, K.L.; Gorman, C.M.; Vehar, G.A.; O'Brien, D.P.; Lawn, R.M.
Thromb. Res. 48, 89-99, 1987
A;Title: Cloning and expression of human tissue factor cDNA.
A;Reference number: A47574; MUID:88100453; PMID:3424286
A;Accession: A47574
A;Molecule type: mRNA
A;Residues: 1-295 <PIS>
A;Cross-references: UNIPARC:UPI000002CD0D; GB:M27436; NID:G339507; PIDN:AAA36734.1; PID:
R;Spicer, E.K.; Horton, R.; Bloem, L.; Bach, R.; Williams, K.R.; Guha, A.; Kraus, J.; Lir
Proc. Natl. Acad. Sci. U.S.A. 84, 5148-5152, 1987
A;Title: Isolation of cDNA clones coding for human tissue factor: primary structure of t
A;Reference number: A94171; MUID:87260946; PMID:3037536
A;Accession: A28320
A;Molecule type: mRNA
A;Residues: 1-295 <SPI>
A;Cross-references: UNIPARC:UPI000002CD0D; GB:J02931; NID:G339501; PIDN:AAA61150.1; PID:
R;Morrissey, J.H.; Fakhrat, H.; Edgington, T.S.
Cell 50, 129-135, 1987
A;Title: Molecular cloning of the cDNA for tissue factor, the cellular receptor for the
A;Reference number: A29062; MUID:87244317; PMID:3297348
A;Accession: A29062
A;Molecule type: mRNA
A;Residues: 1-295 <MOR>
A;Cross-references: UNIPARC:UPI000002CD0D; GB:J02931; NID:G339501; PIDN:AAA61150.1; PID:
A;Note: part of this sequence, including the amino end of the mature protein, was confir
R;Scarpatti, E.M.; Wen, D.; Broze Jr., G.J.; Miletich, J.P.; Flandermeyer, R.R.; Siegel, R.
Biochemistry 26, 5234-5238, 1987
A;Title: Human tissue factor: cDNA sequence and chromosome localization of the gene.
A;Reference number: A29672; MUID:88050796; PMID:2823875
A;Accession: A29672
A;Molecule type: mRNA
A;Residues: 1-259, A', 261-295 <SCA>
A;Cross-references: UNIPARC:UPI000004E645; GB:M16553; NID:G339503; PIDN:AAA61151.1; PID:
R;Bach, R.; Konigsberg, W.H.; Nemerson, Y.
Biochemistry 27, 4227-4231, 1988
A;Title: Human tissue factor contains thioester-linked palmitate and stearate on the cyto
A;Reference number: A37422; MUID:89000604; PMID:3166978
C;Comment: annotation; disulfide bonds and fatty acid binding site
C;Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor f
C;Comment: Expression of tissue factor can be induced in a variety of tissues by certain
C;Genetic:
A;Gene: GDB:F3
A;Cross-references: GDB:119895; OMIM:134390
A;Map position: lp22-1p21
A;Introns: 34/1; 71/2; 138/1; 197/3; 251/1
C;Superfamily: tissue factor
C;Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane
F;1-32/Domain: signal sequence #status predicted <SIG>
F;33-295/Product: tissue factor #status experimental <MAT>
```

F;33-251/Domain: extracellular #status predicted <EXT>
F;252-274/Domain: transmembrane #status predicted <TM>
F;275-295/Domain: intracellular #status predicted <INT>
F;43/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;81-89,218-241/Disulfide bonds: #status experimental
F;156,169/Binding site: carboxylate (Asn) (covalent) #status predicted
F;277/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match 5.3%; Score 156; DB 1; Length 295;
Best Local Similarity 23.7%; Pred. No. 0.00083;
Matches 74; Conservative 54; Mismatches 142; Indels 42; Gaps 17;

QY 1 MRAPGRPALRPLPPLPPLLLALLAAGRAVPCVSGGLPKPA---NITFLSINMKNVLQWT 57
DB 1 METPAMPRV-PRPETAVALTLUG-VVFAQVAGASGTTNVAAYNLTKSTNPKFTILEWE 58

QY 58 PPBGLGVKVTYVQVFIYQKQKWLKNSCRNINRYCDLSAR-TSDYEHQYIYAKKAIW 116
DB 59 P-----KPVNQVYTVQ---ISTKSGDWKSKCFYTTDTECDLTDIEIVKDVKQTYLARVFSYP 111

QY 117 GTKCSKWAESG-----RFYFLETOIGPPREVALTTDEKSISSVLTAPK---WKNRP 165
DB 112 AGNVESTGAGEPLYNSFEFTPYLETNLGQPTIQ-SFEQVGTKNVTVVEDEKTLVRRNN 170

QY 166 EDLPVSMQIY-SNLKYNVSVLNTKSNRTWSQCVTNHTLVLTLWLEPNTLYCVHVESFVPG 224
DB 171 TFL--SLRDVFGKDLIYLYWKSSSSGK-KTAKTNTNEFLIDVDKGENYCFVQAVIPS 227

QY 225 PP--RAAQSEKQACARTLKQDSEFPKAKIFWTV-LPISITVPLFVSMGYSIYRYIHVG- 280
DB 228 RTVNRKSTDPVBC--MGQEKGEFRE--IFYIGAVWFVVIILVILAILSLHKCRKAGV 282

QY 281 ----KEKHPANL 288
DB 283 GOSWKENSPLNV 294

RESULT 15
I39073
interferon alpha-beta receptor, beta subunit long form - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C;Accession: I39073; S59502
R;Domanski, P.; Witte, M.; Kellum, M.; Rubinstein, M.; Hackett, R.; Pitha, P.; Colamonic
J. Biol. Chem. 270, 21606-21611, 1995
A;Title: Cloning and expression of a long form of the beta subunit of the interferon al
A;Reference number: I39073; MUID:95394915; PMID:7665574
A;Accession: I39073
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-515 <RES>
A;Cross-references: UNIPROT:P48551; UNIPARC:UPI000004E646; EMBL:U29584; NID:g993040; PID
R;Lutalla, G.; Holland, S.J.; Cinato, E.; Monneron, D.; Reboul, J.; Rogers, N.C.; Smith
EMBO J. 14, 5100-5108, 1995
A;Title: Mutant USA cells are complemented by an interferon-alpha-beta receptor subunit
A;Reference number: S59501; MUID:960671138; PMID:7588638
A;Accession: S59502
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-150, 'M', 152-515 <LUT>
A;Cross-references: UNIPARC:UPI000012D69B; GB:L41942; NID:g995292; PIDN:AAB46413.1; PID:
C;Keywords: alternative splicing; cytokine receptor

Query Match 5.0%; Score 148.5; DB 2; Length 515;
Best Local Similarity 20.0%; Pred. No. 0.0066;
Matches 112; Conservative 80; Mismatches 210; Indels 157; Gaps 26;

QY 49 NMKNVLQWTPPEGLQG---VKVTYVQYFIYQKQKWLN-KSECRNINRYCDLSAETSDY 104
DB 47 NFRSILSWE----LKNHSIVPHTYLYIMSKPEDLKVVKNCANTRSFCDLTDEWRS- 101

QY 105 EHQQYAKVKAINGTKCSKWAESGRFPFLETQIGPPEVALTTDEKSISSVLTAPKWKRN 164

DB 102 THEAYVTVLEGSGNNTTLFSCSHNFWLAIDMFEPEPEFIVGFTNHNINVVVKPPSIVEEE 161
QY 165 PE-DLPVSMQIY-SNL--KYNVSVLNTKSNRTWSQCVTNHTLVLTLWLEPNTLYCVHVV-- 218
DB 162 LQFDLSLVEESEGIVKHKKEIKGNMSG-----NFTYIDKLIPTNVCVSVYLE 213
QY 219 ----SFVPGPPRRAPQSEKQACARTLKQDSSBF--KAKI-----IFWYVLPISITVPLFS 267
DB 214 HSDEQAVIKSP-----LKTLLPPGQSESAESAKIGGIITVFELIALVLTSTIVTLK 265

QY 268 VMGYSTYRIHVQKXKHPANLILYCNEDKPFVPAEKIVINFINILNISDDSKISHQDM 327
DB 266 WIGYICLR-----NSLPK-----VLNF-----HNFL 286

QY 328 SLLGKSSDVSSLNDPOPSGNLRPPPOEEBVKHLGVASHLMEIFCDSEENTEGTSFTQOES 387
DB 287 A-----WPFNL-PPLEAMDMVEVIYINRKKW---DYNVDESDDTEA 328

QY 388 LSRTIPDPKTVIEYDYVRTTDICAGPEQEQLSLOBEVSTQGTLLLESQAALAVL---GPQ 444
DB 329 APTSGGGYTM--HGLTVRPLGQASATSTESQLIDPESEEPDLPEVDVDELPTMPKDSPO 386

QY 445 TLQYSTPOLQDLPLAQEHDSBEGPEEPSTTLVDWDPTQGLCI-PSLSF----- 497
DB 387 QLELLSGPCERRKSPL-----QDPFPEEDYST-----EGSGRITFNVDLNSVFLRVLD 436

QY 498 DODSECE-----PSEGDGLGEGLLSR-----LYEEPAPD 528
DB 437 DESDDDLEAPLMLSSHLEEMVDPEDPNVQSNHLLASGEGTQPTFPSPSEGLWSEDAFS 496

QY 529 RPPGENET-----YLMQ 540
DB 497 DQSDTSESVDLDGDGYIMR 515

Search completed: April 5, 2006, 11:41:48
Job time : 33.6424 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 5, 2006, 11:30:18 ; Search time 197.134 Seconds
(without alignments)
1979.144 Million cell updates/sec

Title: US-09-745-792A-11

Perfect score: 2947

Sequence: 1 MRAPGRPALRLPLPLLLL.....NETYLMQFMENGLYVQMEN 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2947	100.0	553	1 I20RA_HUMAN	Q9uhf4 homo sapien
2	1770.5	60.1	546	1 I20RA_MOUSE	Q6phb0 mus musculus
3	1041.5	35.3	209	2 Q96SH7_HUMAN	Q96sh7 homo sapien
4	470	15.9	568	2 Q80DF7_TETNG	Q80df7 tetraodon n
5	469	15.9	568	2 Q800G1_TETNG	Q800g1 tetraodon n
6	444	15.1	581	2 Q575Z1_ONCMY	Q575z1 oncorhynch
7	334.5	11.4	236	2 Q5R1W7_BRARE	Q5r1w7 brachydanio
8	315.5	10.7	229	1 I22RA_RAT	Q7tni4 rattus norv
9	310	10.5	263	1 I22RA_HUMAN	Q969j5 homo sapien
10	294.5	10.0	341	2 Q9YGC8_CHICK	Q9ygc8 gallus gall
11	275	9.3	230	1 I22RA_MOUSE	Q80xf5 mus musculus
12	267.5	9.1	349	1 I10R2_MOUSE	Q6l190 mus musculus
13	261	8.9	351	2 Q8VHM7_MOUSE	Q8vhm7 mus musculus
14	257	8.7	574	2 Q8N6P7_HUMAN	Q8n6p7 homo sapien
15	255	8.7	574	2 Q9H822_HUMAN	Q9hb22 homo sapien
16	254.5	8.6	327	2 Q6ZVU9_HUMAN	Q6zv99 homo sapien
17	253.5	8.6	325	1 I10R2_HUMAN	Q80334 homo sapien
18	253.5	8.6	499	2 Q5P1J5_XENLA	Q5p1j9 xenopus lae
19	242.5	8.2	338	2 Q800G2_TETNG	Q800g2 tetraodon n
20	242	8.2	362	2 Q764M7_PIG	Q764m7 sus scrofa
21	240.5	8.2	502	2 Q5U4H8_XENLA	Q5u4h8 xenopus lae
22	239.5	8.1	336	2 Q800E8_TETNG	Q800e8 tetraodon n
23	237	8.0	317	2 Q58CP3_BOVIN	Q58cp3 bos taurus
24	231.5	7.9	581	2 Q80XZ4_MOUSE	Q80xz4 mus musculus
25	225	7.6	575	1 I10R1_MOUSE	Q6l127 mus musculus
26	223.5	7.6	442	2 Q9PVJ9_CHICK	Q9pvj9 gallus gall
27	222.5	7.6	590	1 INAR1_MOUSE	P33896 mus musculus
28	222.5	7.6	590	2 Q80UJ3_MOUSE	Q80uj3 mus musculus
29	220.5	7.5	569	2 Q9YHW0_CHICK	Q9yhw0 gallus gall
30	217.5	7.4	590	2 Q80UR8_MOUSE	Q80ur8 mus musculus
31	215.5	7.3	449	2 Q5XY05_GALLUS	Q5xy05 gallus gall

RESULT 1

I20RA_HUMAN STANDARD; PRT; 553 AA.

AC Q9UHF4; Q6UWA9; Q96SH8;

DT 25-OCT-2004 (Rel. 45, Created)

DT 25-OCT-2004 (Rel. 45, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Interleukin-20 receptor alpha chain precursor (IL-20R-alpha) (IL-20R1)

DE (Cytokine receptor family 2 member 8) (Cytokine receptor ciase-II,

DE member 8) (CRF2-8) (ZCYTOR7).

GN Name=IL20RA; Synonyms=ZCYTOR7; ORFNames=UNQ681/PRO1315;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE (ISOFORM 1).

RA Lok S., Kho C., Jelmberg A., Adams R., Whitmore T., Farrah T.,

RA O'Hara P.;

RT "Homo sapiens cytokine receptor homolog.;"

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

[2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).

RX MEDLINE-22987296; PubMed-12975309; DOI=10.1101/gr.1293003;

RA Clark H.F., Gurney A.D., Abaya E., Baker K., Baldwin D.T., Brush J.,

RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,

RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,

RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,

RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

RA Vandien R.L., Watanabe C., Weand D., Woods K., Xie M.-H.,

RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,

RA Wood W.I., Godowski P.J., Gray A.M.;

RT "The secreted protein discovery initiative (SPDI), a large-scale

RT effort to identify novel human secreted and transmembrane proteins: a

RT bioinformatics assessment.;"

RL Genome Res. 13:2265-2270(2003).

[3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX MEDLINE-22935763; PubMed-14574404; DOI=10.1038/nature02055;

RA Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,

RA Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,

RA Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Alnough R.,

RA Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,

RA Babbage A.K., Baguley C.L., Bailey J., Banerjee R., Barker D.J.,

RA Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,

RA Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown J.Y.,

RA Burford D.C., Burrell W., Burton J., Carder C., Carter N.P.,

RA Chapman J.C., Clark S.Y., Clark G., Clegg S., Cobley V.,

RA Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J.,

RA Cullley K.M., Dhali P., Davies J., Dunn M., Earthrowl M.E.,

RA Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,

RA Frankland J., French L., Garner P., Garnett J., Ghorri M.J.,

RA

RA Gilby L.M., Gillson C.J., Glithero R.J., Grafham D.V., Grant M.,
RA Gribble S., Griffiths C., Griffiths M.N.D., Hall R., Halls K.S.,
RA Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcott R.,
RA Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,
RA Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,
RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,
RA Lawlor S., Leongamornlert D.A., Levertha M., Lloyd C.R., Lloyd D.M.,
RA Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi M.,
RA MacLennan G.L., Matthews L., McCann O.T., McLaren S.J., McLay K.,
RA McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T.,
RA Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Patel R.,
RA Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S., Plumb R.W.,
RA Porter K.M., Ramsey Y., Ranby S.A., Rice C.M., Ross M.T., Searle S.M.,
RA Sehra H.K., Sheridan E., Skuce C.D., Smith S., Smith M., Spraggon L.,
RA Squares S.L., Steward C.A., Sycamore N., Tاملين-Hall G., Tester J.,
RA Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B.,
RA Wall M., Wallis J.M., West A.P., White S.S., Whitehead S.L.,
RA Whittaker H., Wild A., Willey D.J., Wilmer T.E., Wood J.M., Wray P.W.,
RA Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,
RA Durbin R., Hubbard T., Sulston J.E., Dunham I., Rogers J., Beck S.;
RT "The DNA sequence and analysis of human chromosome 6.";
RL Nature 425:805-811(2003).
RN [4]
RP PROTEIN SEQUENCE OF 30-44.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RY Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
RN [5]
RP SUBUNIT, LIGAND-BINDING, AND TISSUE SPECIFICITY.
RX MEDLINE=21097717; PubMed=11163236; DOI=10.1016/S0092-8674(01)00187-8;
RA Blumberg H., Conklin D., Xu W.F., Grossmann A., Brender T.,
RA Carollo S., Eagan M., Foster D., Haldeman B.A., Hammond A., Haugen H.,
RA Jelinek L., Kelly J.D., Madden K., Maurer M.F., Parrish-Novak J.,
RA Prunkard D., Sexson S., Sprecher C., Waggle K., West J.,
RA Whymore T.E., Yao L., Kuechle M.K., Dale B.A., Chandrasekher Y.A.;
RT "Interleukin 20: discovery, receptor identification, and role in
RT epidermal function.";
RL Cell 104:9-19(2001).
RN [6]
RP LIGAND-BINDING.
RX PubMed=11564763;
RA Dumoutier L., Leemans C., Lejeune D., Kotenko S.V., Renaud J.-C.;
RT "STAT activation by IL-19, IL-20 and mda-7 through IL-20 receptor
RT complexes of two types.";
RL J. Immunol. 167:3545-3549(2001).
RN [7]
RP SUBUNIT, AND LIGAND-BINDING.
RX PubMed=12351624; DOI=10.1074/jbc.M205114200;
RA Parrish-Novak J., Xu W., Brender T., Yao L., Jones C., West J.,
RA Brandt C., Jelinek L., Madden K., McKernan P.A., Foster D.C.,
RA Jaspers S., Chandrasekher Y.A.;
RT "Interleukins 19, 20, and 24 signal through two distinct receptor
RT complexes. Differences in receptor-ligand interactions mediate unique
RT biological functions.";
RL J. Biol. Chem. 277:47517-47523(2002).
RN [8]
RP SUBUNIT, AND LIGAND-BINDING.
RX PubMed=14580208; DOI=10.1021/bi0354583;
RA Pletnev S., Magracheva E., Kozlov S., Tobin G., Kotenko S.V.,
RA Wlodawer A., Zdanov A.;
RT "Characterization of the recombinant extracellular domains of human
RT interleukin-20 receptors and their complexes with interleukin-19 and
RT Biochemistry 42:12617-12624(2003).
RN [9]
RP SUBUNIT, LIGAND-BINDING, AND TISSUE SPECIFICITY.
RX PubMed=14764663;
RA Sheikh F., Baurin V.V., Lewis-Antes A., Shah N.K., Smirnov S.V.,
RA Anantha S., Dickensheets H., Dumoutier L., Renaud J.-C., Zdanov A.,
RA Donnelly R.P., Kotenko S.V.;
RT "IL-26 signals through a novel receptor complex composed of IL-20

receptor 1 and IL-10 receptor 2.";
RL J. Immunol. 172:2006-2010(2004).
CC -!- FUNCTION: The IL20RA/IL20RB dimer is a receptor for IL19, IL20 and
CC IL24. The IL20RA/IL20RB dimer is a receptor for IL26.
CC -!- SUBUNIT: Heterodimer with IL20RB and heterodimer with IL10RB.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9UHF4-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9UHF4-2; Sequence=VSP_011497, VSP_011498;
CC -!- TISSUE SPECIFICITY: Widely expressed with highest levels in skin
CC and testis and high levels in brain. Highly expressed in psoriatic
CC skin.
CC -!- SIMILARITY: Belongs to the type II cytokine receptor family.
CC -!- SIMILARITY: Contains 2 fibronectin type-III domains.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF184971; AAF01320.1; -; mRNA.
CC EMBL; AY358883; AAQ89242.1; -; mRNA.
CC EMBL; AL135902; CAC38375.1; -; Genomic_DNA.
CC HSSP; P13726; 2HFT.
CC DR Ensembl; ENSG00000016402; Homo sapiens.
CC DR HGNC; HGNC:6003; IL20RA.
CC DR MIM; 605620; -.
CC DR InterPro; IPR000282; Cytok receptor_2.
CC DR InterPro; IPR003961; FN III.
CC DR InterPro; IPR001187; Tissue_factor.
CC DR Pfam; PF01108; Tissue_fac; 1.
CC DR PROSITE; PS00853; FN3; FALSE NEG.
CC KW Alternative splicing; Direct protein sequencing; Glycoprotein;
CC Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 29
FT CHAIN 30 553 Interleukin-20 receptor alpha chain.
FT TOPO_DOM 30 250 Extracellular (Potential).
FT TRANSMEM 251 271 Potential.
FT TOPO_DOM 272 553 Cytoplasmic (Potential).
FT DOMAIN 37 136 Fibronectin type-III 1.
FT DOMAIN 138 237 Fibronectin type-III 2.
FT COMEPIAS 353 356 Poly-Glu. (Potential).
FT CARBOHYD 42 42 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 83 83 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 91 91 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 182 182 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 191 191 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 200 200 N-linked (GlcNAc. . .) (Potential).
FT DISULFID 87 95 By similarity.
FT DISULFID 215 236 By similarity.
FT VARSPPLIC 1 111 Missing (in isoform 2).
FT VARSPPLIC 112 135 VKAIWGTCKSKWAESGRFYPFLET -> MSYNGLHQRFKE
FT LKILTLCSISS (in isoform 2).
FT /FTId=VSP_011498.
FT CONFLICT 259 259 I -> V (in Ref. 2).
FT CONFLICT 382 382 F -> L (in Ref. 2 and 3).
FT SEQUENCE 553 AA; 625534 MW; 7C23C8543B114659 CRC64;
SQ
Query Match 100.0%; Score 2947; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.3e-196;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRAPGRPALRPLPPLPPLLLLLLAAAPWGRAVPCVSGGLPKPANITFLSINKNVLTPTPE 60
Db 1 MRAPGRPALRPLPPLPPLLLLLLAAAPWGRAVPCVSGGLPKPANITFLSINKNVLTPTPE 60
QY 61 GLQGVKVTYQVFIYFGQKKWLKNSCRINRTYCDLSAETSDYEHQYAKVAIWGTC 120
|||||

Db 61 GLOGVYTVYQVFIYQKKWLNKSECRNINRTYCDLSAETSYEHQYAKVKAIWGTC 120

QY 121 SKWAESGRFFPFLTEITGPPPEVALTTDEKSIISVLTAPKWKKNPBDLPVSMQOIYSNLK 180

Db 121 SKWAESGRFFPFLTEITGPPPEVALTTDEKSIISVLTAPKWKKNPBDLPVSMQOIYSNLK 180

QY 181 YNVSVLNTKSNRTWSQCVNTHLTLVLTWLEPNTLYCVHVESFVPGPRRAQPSKQCARTL 240

Db 181 YNVSVLNTKSNRTWSQCVNTHLTLVLTWLEPNTLYCVHVESFVPGPRRAQPSKQCARTL 240

QY 241 KDOSSEFKAKIIFWYVLPISITVFLFSVMGYSYIRYIHVKEKHPANLILYNEFDKRF 300

Db 241 KDOSSEFKAKIIFWYVLPISITVFLFSVMGYSYIRYIHVKEKHPANLILYNEFDKRF 300

QY 301 FVPAEKIVNFIITNLSDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQSEEVKHL 360

Db 301 FVPAEKIVNFIITNLSDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQSEEVKHL 360

QY 361 GYASHLMEIFCDSEENTEGTSFTQBSLSRTIPDPKTVIEYDVRTTDCAGPERQELS 420

Db 361 GYASHLMEIFCDSEENTEGTSFTQBSLSRTIPDPKTVIEYDVRTTDCAGPERQELS 420

QY 421 LQBEVSTQGTLLSQALAVLGQTLQYSTPQLDPLAQHSTDSGPEEPSTTLV 480

Db 421 LQBEVSTQGTLLSQALAVLGQTLQYSTPQLDPLAQHSTDSGPEEPSTTLV 480

QY 481 DNDPQTRGLCIPSLSSFDQDSECEPSEGGDLGEGLLSRLYEAPDRPPGNETYLMQ 540

Db 481 DNDPQTRGLCIPSLSSFDQDSECEPSEGGDLGEGLLSRLYEAPDRPPGNETYLMQ 540

QY 541 FMEEWGLYQVMEN 553

Db 541 FMEEWGLYQVMEN 553

RESULT 2

I20RA_MOUSE

ID I20RA_MOUSE STANDARD; PRT; 546 AA.

AC Q6PHB0; Q8BW64;

DT 25-OCT-2004 (Rel. 45, Created)

DT 25-OCT-2004 (Rel. 45, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Interleukin-20 receptor alpha chain precursor (IL-20R-alpha) (IL-20R1).

DE 20R1).

GN Name=IL20ra;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidae; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

[1]

RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RC STRAIN=C57BL/6J; TISSUE=Oviduct;

RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

RA Dalla E., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglott D.R., Malcais L., Marchionni L., McKenzie L., Miki H.,

RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Miyazaki A., Sakai K., Sakaki D., Shibata K., Shinagawa A.,

RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Birney E., Hayashizaki Y.;

RT "Analysis of the mouse transcriptome based on functional annotation of

60,770 full-length cDNAs.";

RL Nature 420:563-573 (2002).

[2]

RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RP STRAIN=129; TISSUE=Mammary tumor;

RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uedin T.B., Teohiyuki S., Carninci P., Prange C.,

RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC -!- FUNCTION: The IL20RA/IL20RB dimer is a receptor for IL19, IL20 and

IL24. The IL20RA/IL20RB dimer is a receptor for IL26 (By

similarity).

CC -!- SUBUNIT: Heterodimer with IL20RB and heterodimer with IL10RB (By

similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -!- SIMILARITY: Belongs to the type II cytokine receptor family.

CC -!- SIMILARITY: Contains 2 fibronectin type-III domains.

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CC

CC EMBL; AK054215; BAC35695.1; -; mRNA.

CC EMBL; BC056628; AAH56628.1; -; mRNA.

DR HSSP; P13726; 2HFT.

DR InterPro; IPR000282; Cytok receptor_2.

DR InterPro; IPR003961; FN_III.

DR InterPro; IPR001187; Tissue_factor.

DR Pfam; PF01108; Tissue_fac; 1.

DR PROSITE; PS00853; FN3; FALSE NEG.

KW Glycoprotein; Receptor; Repeat; Signal; Transmembrane.

FT SIGNAL 1 32 Potential.

FT CHAIN 33 546 Interleukin-20 receptor alpha chain.

FT TOPO_DOM 33 253 Extracellular (Potential).

FT TRANSMEM 254 274 Potential.

FT TOPO_DOM 275 546 Cytoplasmic (Potential).

FT DOMAIN 33 142 Fibronectin type-III 1.

FT DOMAIN 143 251 Fibronectin type-III 2.

FT CARBOHYD 45 45 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 86 96 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 94 94 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 185 185 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 203 203 N-linked (GlcNAc...) (Potential).

FT DISULFID 90 98 By similarity.

FT DISULFID 218 239 By similarity.

FT CONFLICT 145 145 V -> I (in Ref. 2).

SQ	SEQUENCE	546 AA; 61978 MW; E7EC07DA2D49AF7F CRC64;
	Query Match	60.1%; Score 1770.5; DB 1; Length 546;
	Best Local Similarity	63.3%; Pred. No. 1.1e-114;
	Matches	352; Conservative 51; Mismatches 140; Indels 13; Gaps 3;
QY	1	MRAPGRPALRPLPLPPL---LLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWT 57
Db	1	MHTPGTPAPGHPDPPLLLTLTLLLAASGRAVPCVFCGLPKPTNITFLSINMKNVLHW 60
QY	58	PREGLOGKVTYVQYFYIGQKKWLNKSECRNINRTYCDLSAETSDYEHQYAKVAIWG 117
Db	61	PPESLHGVEVTYVQYFYIGQKKWLNKSECRNINRTYCDLSVETSDYEHQYAKVAIWE 120
QY	118	TKCSKWAESGRFPFPLETOIGPPEVALTTDEKSIISVLTAPKWKKNPEDLPVSMQOIYS 177
Db	121	ARCSEWAETERFPFLETOUSPPEVALTTGEKSIISALTAPKWKKNPODHTVSMQOIYP 180
QY	178	NLYKYNVSLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVSVFVPGPPRRAPQSEKQCA 237
Db	181	NLYKYNVSVNTKSNRTWSQCVTNSTLVLSWLEPNTLYCVHVSVLVPGLPMPSPKQCI 240
QY	238	RILKQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVCKEKHPANLILYGNED 297
Db	241	STLEVQTSAAKAKVIEFYVFLTSVIVFLFSAIGLYVYRIHVCKEKHPANLILYRNEIG 300
QY	298	KAFFVPAEKIVNFITLNTSDSKISHODMSLLGKSSDVSLNDPOPSGNLRPPQEEEV 357
Db	301	TRVFEETITLNFITFSDDDTKISPKDMNLLDKSSDISVNDPBNNEAEPHWEVEVG 360
QY	358	KHLGYASHLMEIFCDSEENTGFTSQBSLSRTIPDPKTVIEYEDVTRTTDICAGPEBQ 417
Db	361	QHLGSCSSHLMDAVCGAEQRDGTSLTQHGWLNSTIPTGETDTEPYQKVLSD--FYGEGEI 418
QY	418	ELSLQEVSTQGTLLSQALAVLGQTLOYSTYPOLDLPLAQHTDSEGEPEEPST 477
Db	419	QLSCEPE-----EAARTEKISEPLVTSANLDPQLEDHLHGQHTVSEDGPEBETSI 470
QY	478	TLVDWDPOQTRGLCIPSLSDQSECEPSEGGGLGELLSRLYEAPAPDRPPGNETY 537
Db	471	TVVDWDPOQTRGLCIPSLPIFGRPENYGHYERDQLLEGGLLSRLYENQAPDKPENENC 530
QY	538	LMQFMEEWGLYQVOMN 553
Db	531	LTRFMEEWGLHWQMES 546
RESULT 3		
Q96SH7	HUMAN	
ID	Q96SH7_HUMAN	PRELIMINARY; PRT; 209 AA.
AC	Q96SH7	
DT	01-DEC-2001	(TrEMBLrel. 19, Created)
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)
DE	OTTHUMP0000017281.	
GN	Name=IL20RA; ORFName=RP11-204P2.1-003;	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;	
OC	Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]_	TaxID=9606;
RP	NUCLEOTIDE SEQUENCE.	
RA	Griffiths C.;	
RL	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.	
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).	
DR	EMBL; AL135902; CAC38376.1; -; Genomic_DNA.	
DR	HSSP; P13726; 2HT.	
DR	Ensembl; ENSG0000016402; Homo sapiens.	
DR	GO; GO:0016021; C:integral to membrane; IEA.	
DR	GO; GO:0016020; C:membrane; IEA.	
DR	GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.	
DR	GO; GO:0004872; F:receptor activity; IEA.	

DR	InterPro; IPR000282; Cytok_receptor_2.	
KW	Receptor; Transmembrane.	
SQ	SEQUENCE	209 AA; 23616 MW; 467AB77BE3840361 CRC64;
	Query Match	35.3%; Score 1041.5; DB 2; Length 209;
	Best Local Similarity	91.7%; Pred. No. 1.7e-64;
	Matches	200; Conservative 1; Mismatches 4; Indels 13; Gaps 3;
QY	1	MRAPGRPALRPLPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPE 60
Db	1	MRAPGRPALRPLPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPE 60
QY	61	GLQGVKVTYVQYFYIGQKKWLNKSECRNINRTYCDLSAETSDYEHQYAKVAIWGTC 120
Db	61	GLQGVKVTYVQYFYIGQKKWLNKSECRNINRTYCDLSAETSDYEHQYAKVAIWGTC 120
QY	121	SKWAESGRFPFLETOIGPPEVALTTDEKSIISVLTAPKWKKNPEDLPVSMQOIYSNLK 180
Db	121	SKWAESGRFPFLETOIGPPEVALTTDEKSIISVLTAPKWKKNPEDLPVSMQOIYSNLK 180
QY	181	YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHV 218
Db	181	YNVSVLNTKSNRTVS-----LKW--NGAY-IHV 205
RESULT 4		
Q800F7	TETNG	
ID	Q800F7_TETNG	PRELIMINARY; PRT; 568 AA.
AC	Q800F7	
DT	01-JUN-2003	(TrEMBLrel. 24, Created)
DT	01-JUN-2003	(TrEMBLrel. 24, Last sequence update)
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)
DE	Helical cytokine receptor CRFB8.	
GN	Name=crfb8;	
OS	Tetraodon nigroviridis (Green puffer).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Actinopterygii; Neoceratogryll; Teleostei; Euteleostei; Neoteleostei;	
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;	
OC	Tetraodontidae; Tetraodontidae; Tetraodon.	
OX	NCBI_TaxID=99883;	
RN	[1]_	TaxID=99883;
RP	NUCLEOTIDE SEQUENCE.	
RA	Lutfalla G., Roest Crolius H., Stange-Thomann N., Jaillon O.,	
RA	Mogensen K., Monneron D.;	
RT	"Comparative genomic analysis reveals independent expansion of a	
RT	lineage-specific gene family in vertebrates: The class II cytokine	
RT	receptors and their ligands in mammals and fish."	
RL	BMC Genomics 4:29-29(2003).	
DR	EMBL; AJ544894; CAD67782.1; -; Genomic_DNA.	
DR	GO; GO:0016020; C:membrane; IEA.	
DR	GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.	
DR	GO; GO:0004872; F:receptor activity; IEA.	
DR	InterPro; IPR000282; Cytok_receptor_2.	
KW	Receptor.	
SQ	SEQUENCE	568 AA; 63848 MW; A8A38DC3BF78ABE2 CRC64;
	Query Match	15.9%; Score 470; DB 2; Length 568;
	Best Local Similarity	26.1%; Pred. No. 4.7e-24;
	Matches	158; Conservative 106; Mismatches 233; Indels 108; Gaps 23;
QY	17	LLLLLAAAPWGRAVPC-VSGGLPKPANITFLSINMKNVLQWTPPEGLQGVKVTYVQYFI 75
Db	4	VLLLDLA-----AFQCLVLSASLPSPTSVFIAISVNLNVLEWTPGNDTPS-NATFTVQYAI 57
QY	76	YQOK-----KWLNKSECRNINRTYCDLSAETSDYEHQYAKVAIWGTCSEWASGRF 129
Db	58	YGDSDKRRSVRRALQRCNTAQSCWCDLSNQTDLDEAYARVRAESKAWGWSQTRRF 117
QY	130	YPELETQIGPPEVALTTDEKSIISVLTAPKWKKNPEDLPVSMQOIYSNLKYNVSVLNTK 189
Db	118	DPKSDITFGPPQMSVEVENSALIVTKGPMRYOPNFQMPAVSNATYIPHHMYNLISNTY 177
QY	190	SNRTWSQCVTNHTLVLTWL-----EPNTLYCVHVSVFVGPVPRRAQPSKQCAITLQDQ 243

178	RNK	-----TSHFILSSGLYKHHLAENKEYCFVKAKFLAMPVQCOSSEWQCITPTDP	231
244	SSEFKAKI	FWYVVISITVFLFVSVMGYSIYRIYHVGKEKHPANLILYGNEDFKGFVP	303
232	MYRHLQWV	VSVVPL--VCVYMGVTGSGILYQYLMGICQKTPQLDQAFNQHSILF--P	288
304	AEKIVINF	ITLNISSDKISHQMSLLGCKSSDVSLNDQPQSGNLRPQPEEEVYHGLGYA	363
289	LENTSLNAIT	--SISPADTMTDQ-----RFKDPPOQYAVHLPQ--ETVYNCDDR	333
364	SHLMEIFC	DSEBTEGTSPTQESLSRTIPDPKTVIEYEVDRT-----TDICAGPE	415
334	SIYGLVSAT	SHNGEGNPTKHKOHSSGGYAPQTMSSLQRPFPRLKHSAAATSSAP--	392
416	EQELSLOE	EVSTQGTLLSQALAVLGPQTLOYSYTPQLQDLPL-----AQEHT--	465
393	EQTAPQSP	LANKVMKLK--ELGVILGMEDKSN-----ELEPLFGYAAQNTTAFAA	445
466	-----DSB--	EGPEERP-----GTTLVMDPDPOTGRLCIPSLSSF-----DQDSEGC	504
446	HSEQSEF	RLADNEKKGDCHEEEERVGTIIFIDMDPSKNKLVLDELTKWYVRENKXENGW	505
505	EPSEG-----	DGLGEGLLSLRYEEPAPDR-----PPGENETYLMQFMEEBGLY	548
506	EATKGAAB	EENVMWGGELLSGGVCVQASDKVLAPELTGLGRDPEGAGK--VRDILTKKNLV	563
549	VQMEN	553	
564	IPMED	568	

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RESULT 5
Q800GI_TETNG Q800GI_TETNG PRELIMINARY; PRT; 568 AA.
ID Q800GI_TETNG PRELIMINARY; PRT; 568 AA.
AC Q800GI;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Helical cytokine receptor CRFB8.
DE Names=crfb8;
GN Tetraodon nigroviridis (Green puffer).
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OC NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lutfalla G., Roest Crolius H., Stange-Thomann N., Jaillon O.,
RA Mogenssen K., Monneron D.;
RT "Comparative genomic analysis reveals independent expansion of a
RT lineage-specific gene family in vertebrates: The class II cytokine
RT receptors and their ligands in mammals and fish.";
RN BMC Genomics 4:29-29(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Lutfalla G.;
RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AJ2544911; CAD67769.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000282; Cytok_receptor_2.
KW Receptor.
KW SEQUENCE 568 AA; 63834 MW; FE3AA901C0C31E93 CRC64;
SQ

```

Query Match 15.9%; Score 469; DB 2; Length 568;
Best Local Similarity 26.1%; Pred. No. 5.5e-24;
Matches 159; Conservative 105; Mismatches 234; Indels 108; Gaps 23;

Db	4	VLLDLA-----AFQCLVSLASLPSTSVFTIASVNLNRNVLEWTPGNDTPS-NATFTVQVAI	57
Qy	76	YGQK-----KWLNKSECRNIRTYCDLSAFTSDYEHQYAKVAIWGTKCSKWAESGRF	129
Db	58	YGSDKRRSVRWALQRCTNTAQSCWCDLSNQTRDLEEAYARVRAESRKAWSGWSQTRRF	117
Qy	130	YPFLETOIGPEVALITTDKSIISVVLTAPEKXKNPDLPSYMQOIIYNLKNVSVLNTK	189
Db	118	DPKSDTITFGPPQMSVEVENSNAIVTVKGPMPKYQFNQFPAVSMATYIYPHMYNLNIRNTY	177
Qy	190	SNRTSQCVTNHTLVLTWL-----EPNTLYCVHVSEFVPPRRRAQPSKQCARLTQDQ	243
Db	178	RNK-----TSHFILSSGLYKHLAEYNKECFPSVKAKFLAMPVQCQSEWQCITPTDP	231
Qy	244	SSEPKAKIIFYWVLPISITVPLFSVMGYSVIYRYIHVGKEKHPANILIIYGNHFDKRFVFP	303
Db	232	MVRHLQWVSVIVVPL-VCVYIMGVTGSILYQYLMIGIGOKTFOILDQAFSNQHSLLF--P	288
Qy	304	AEKIVINFITLINSDDSKI SHODMSLLGKSDVSSLNDPQSGNLRPPQBEHEEVKHLGVA	363
Db	289	LERTSLNAIT-SISPADTMTDQ-----RFKDPPOQYAVHLFQ--ETVYNCDDR	333
Qy	364	SHLMEIFCDSEENTEGTSFTQGESLRTIPDPKTVIEYDVRT-----TDICAPGE	415
Db	334	SIYGLVSATSHNGEGGNPIKHQKNHSGSVYAPQTMSSLQRFPHFLQKHSATAESSAP-	392
Qy	416	EQELSLQEEVSTQGTLLSQAALVLPQTLOYSYTPQOLDPL-----AQEHT-----	465
Db	393	EQTAPFQSPNLVVKMLKELGVIA-LGWEDKSN-----ELEPLFSYAAQNTNTAFAA	445
Qy	466	-----DSE---EGPREP-----STTLVDMDPQTRGLCIISLSF-----DQDSECC	504
Db	446	HSBQSEFLADNEKNGDGHBEESERVGTIFIDWDPKSNKLVLBELTKWIVRENPENGW	505
Qy	505	EPSEG-----DGLGEEGLLSRLYEEBPADR-----PPGENETYLMQFMEEWGLY	548
Db	506	EATKGAAEEENVMGELLSGGVCVQASDKEVLAPTELGRDPPEGAGK--VRDILTKNVL	563
Qy	549	QVMEN	553
Db	564	IPMED	568

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RESULT 6
Q57521.1 ONCMY PRELIMINARY; PRT; 581 AA.
ID Q57521.1 ONCMY PRELIMINARY; PRT; 581 AA.
AC Q57521;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Interleukin-20 receptor alpha.
GN Names:il20ra;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID=8022;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wang T., Secombes C.J.;
RA "Sequence analysis of rainbow trout genes modulated by bacterial
RT infection."
RT infection."
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ555870; CAD88596.1; -; mRNA.
KW Receptor.
SQ SEQUENCE 581 AA; 66000 MW; 073EA998CEPF9F5A3 CRC64;

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[illegible]

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Db 5 LYIISLWTA VVSVDV - SVARPKGVHFNMSNLRNIVKWHFCKDPN-DTNYTVEYAIYGD 62
QY 80 -----KWLKNSKERNINRTYCDLSAETSDYEHQYAKVKAIWCTKCKSWAESGR-FY 130
Db 63 MDGGARRVRLKKKCRDIPQWCDLSNETTDLDEGYFARVRAIKGNKSGSKWTLTEKSP 122
QY 131 PLETOIGPPEVALTTDEKSIISVLTAPKWKRNPELPSVMOOIYSNLKYNVSVLNTKS 190
Db 123 PRADTTFGPPLVKLVVKENSVTVMKGPMEWKNTGNMTKEYSLLLKFPQMTYNLSVVDN 182
QY 191 NRTWSOCVNTHTLVLTWLBENTLYCVHVESFVGPMPRAQPSKQCARLTQKOSSEFKAK 250
Db 183 NKTQHTFVNRSPEYRLLAYETOYCFSAKAVLSLLFACHASWQCLTTSKDPFYQQLLL 242
QY 251 IIFWYVLPISITVFLFSVMGYSIYRIHVCKEHPANLILYGNFEDKREFFVPAEKIVN 310
Db 243 MLGAVVPSVICLFLMLILVGLCYHVFVCGNKQKSPF-FLEISDIPNPPQTFCEQAVTN 301
QY 311 FITLNISSDKS-----ISHQ----- 325
Db 302 VVLVNAKPMEMPINPNTILALIQHSEGEPILPYAAQQAQPGREDCEGSGWEDDFEAQ 361
QY 326 ----DMSLLGKSDVSLNDPQSGNLRPQEBEEVHGLVYAS-HL----- 366
Db 362 EPLEYFGICASPRIKIPEMRESEASHS-----EETPLLHLQVNMHIAQRSAPCSQGP 416
QY 367 ---MEIFCDSEENECTSFTQOESLSRTIPDPKTVIEYVDVRTT---DICAGPESQELS 420
Db 417 LRFMPULSLGKMGESTSYKEPRVGYAP-----QHFSVRETPEVDFWEDKABEPOS 469
QY 421 LOBEVSTQGLLESQAALAVLGPQTLYQS-----YTPQLQDLPLAQEHTDSEEGPBEPS 476
Db 470 YPSEYETQSNR-----RGTPQLRLSQVNLRYTQRHTLFPQSEEEEDGSG----- 514
QY 477 TTLVWDNDPOTGRLCIPSLS-----SFDQDSECE--PSEGDGLGSEGLLSRLIYEPAP 528
Db 515 -NCVDSMTPTGIQLIPLLSKPIPEVNVNRELEQVEILPS-----VVVROSEE---- 560
QY 529 RPPGENETVLMQPMESWGLYVQME 552
Db 561 ---CEGESDLTELQNNWSLVINME 581

RESULT 7
QSR1W7_BRARE PRELIMINARY; PRT; 236 AA.
AC QSR1W7;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Novel protein (Fragment).
GN Name=OTTDARP0000004673; ORNNames=CH211-272F15.1-001;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Pelan S.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX072559; CA111965.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR InterPro; IPR000282; Cytok_receptor_2.
FT NON TER 236
SQ SEQUENCE 236 AA; 26811 MW; 11A5DFB03860F85E CRC64;

Query Match 11.4%; Score 334.5; DB 2; Length 236;
Best Local Similarity 36.2%; Pred. No. 3.7e-15;
Matches 81; Conservative 41; Mismatches 91; Indels 11; Gaps 4;

QY 28 RAVPCVSG-GLPRPANITFLSINKNVLOWTPPEGLQGVKVTYTVQYFIYG-----Q 78
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Db 14 RALSASSADGPPEPRDVHFYSESLRNVVKTAGHGSPTDV-YTVEYAIYGADEKIQE 72
QY 79 KWLKNSKERNINRTYCDLSAETSDYEHQYAKVKAIWCTKCKSWAES-GRFPFLETQI 137
Db 73 VRMPVDQICISVQTECDVSQETFDLRDIFYARVRATSKHGQSVWSESIGRFRPLSDTVL 132
QY 138 GPPEVALTTDEKSIISVLTAPKWKRNPELPSVMOOIYSNLKYNVSVLNTKSNRTWSQC 197
Db 133 GAPLVDTVTRQNHIDITLKGPFWRMKMKESLWKIIPNMIYKVSFVNSRNRDTPVR 192
QY 198 VTNHTLVLTWLBENTLYCVHVESFVGPMPRAQPSKQCARLTQK 241
Db 193 LTNGSLSLGELEFSTQFCVVAQAQSESIPLSVIPSKQCVHTPK 236

RESULT 8
I22RA_RAT STANDARD; PRT; 229 AA.
AC Q7TNI4;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DE Interleukin-22 receptor alpha-2 chain precursor (IL-22R-alpha-2)
DE (Interleukin 22-binding protein) (IL22BP) (Cytokine receptor family
DE type 2, soluble 1) (CRF2-S1).
GN Name=IL22ra2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=Sprague-Dawley; TISSUE=Spleen;
RX PubMed=15201862; DOI=10.1038/sj.gene.6364104;
RA Weiss B., Wolk K., Gruenberg B.H., Volk H.D., Sterry W., Asadullah K.,
RA Sabat R.;
RT "Cloning of murine IL-22 receptor alpha 2 and comparison with its
RT human counterpart.";
RL Genes Immun. 5:330-336 (2004).
CC -!- FUNCTION: Receptor for IL-22. Binds to IL-22, prevents interaction
CC with the functional IL-22R complex and blocks the activity of IL-
CC 22 (in vitro). May play an important role as an IL-22 antagonist
CC in the regulation of inflammatory responses.
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- SIMILARITY: Belongs to the type II cytokine receptor family.
CC -!- SIMILARITY: Contains 2 fibronectin type-III domains.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AJ555485; CAD88475.1; -; mRNA.
CC HSSP; P13726; 1JPS.
CC DR Ensembl; ENSRNOG00000012259; Rattus norvegicus.
CC InterPro; IPR000282; Cytok_receptor_2.
CC InterPro; IPR003961; FN_III.
CC PROSITE; PS50853; FN3; FALSE NEG.
KW Glycoprotein; Receptor; Repeat; Signal.
FT SIGNAL 1 19 By similarity.
FT CHAIN 20 229 Interleukin-22 receptor alpha-2 chain.
FT DOMAIN 23 127 Fibronectin type-III 1.
FT DOMAIN 128 229 Fibronectin type-III 2.
FT CARBOHYD 54 54 N-linked (GlcNAc...) (Potential).
FT DISULFID 204 225 By similarity.
SQ SEQUENCE 229 AA; 26722 MW; 5CFD37652A99365 CRC64;

Query Match 10.7%; Score 315.5; DB 1; Length 229;
Best Local Similarity 33.8%; Pred. No. 7.4e-14;
Matches 76; Conservative 32; Mismatches 108; Indels 9; Gaps 4;
```

QY 17 LLLLLLAAPNGRAVPCVSGGLPKPANITFLSINKNKVLQWTPPEGLOGVKVTVYQVFIY 76
 DB 9 LLIMLLTATETOPAHVS---LKPQKVOFOSRPNHNLHWPONGNSLTSNGSVFVQYKTY 65
 QY 77 GQKWLKNSCRNINRNYCDLSAETSDEYHQYAKVAIWGTCSCWAEGSRFPVPLETQ 136
 DB 66 GQGQKDKNDGWTGTFALFCDLTKETLDPYEPYGRVMAMAGSVSEWTRTPRTPWETK 125
 QY 137 IGPEVALTTDEKSIISVVLFAPEKKNKPNEDLPVSMQOIYSNLKYNVSLNT---KSNRT 193
 DB 126 LDPPVVTITRVNASLRVLRPPELPHRNQTKNTMENY-ILVYRVSIINNSLEKQKA 184
 QY 194 WSQCVNHTLVLTWLENTLYCVHVESFVGPFPRAQPSKQCAR 238
 DB 185 YEG--TORAVEIOGLTHPCYCVVAEMYQPMFRRSPRSKERCVO 227

RESULT 9
 ID 122RA HUMAN STANDARD; PRT; 263 AA.
 AC Q96J05; Q6UW01; Q96A41; Q96QR0;
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Interleukin-22 receptor alpha-2 chain precursor (IL-22R-alpha-2)
 DE (Interleukin 22-binding protein) (IL22BP) (Cytokine receptor family
 DE class II member 1) (CRF2-10) (Cytokine receptor family type 2,
 DE soluble 1) (CRF2-S1).
 GN Name=IL22RA2; ORFName=UNG5793/PRO19598/PRO19822;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.
 RC TISSUE=Mammary gland, and placenta;
 RX MEDLINE=21518574; PubMed=11607789; DOI=10.1038/sj.gene.6363786;
 RA Gruenberg B.H., Schoenemeyer A., Weiss B., Toschi L., Kunz S.,
 RA Wolk K., Asadullah K., Sabat R.;
 RT "A novel, soluble homologue of the human IL-10 receptor with
 RT preferential expression in placenta.";
 RL Genes Immun. 2:329-334(2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1; 2 AND 3), AND FUNCTION.
 RX MEDLINE=21286453; PubMed=11390454;
 RA Kotenko S.V., Izotova L.S., Mirochnitchenko O.V., Esterova E.,
 RA Dickensheets H., Donnelly R.P., Pestka S.;
 RT "Identification, cloning, and characterization of a novel soluble
 RT receptor that binds IL-22 and neutralizes its activity.";
 RL J. Immunol. 166:7096-7103(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), AND FUNCTION.
 RC TISSUE=Mammary gland;
 RX PubMed=11390453;
 RA Dumoutier L., Lejeune D., Colau D., Renaud J.-C.;
 RT "Cloning and characterization of IL-22 binding protein, a natural
 RT antagonist of IL-10-related T cell-derived inducible factor/IL-22.";
 RL J. Immunol. 166:7090-7095(2001).
 RN [4]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 2), FUNCTION, AND TISSUE SPECIFICITY.
 RX MEDLINE=21396532; PubMed=11481447; DOI=10.1073/pnas.171303198;
 RA Xu W., Presnell S.R., Parrish-Novak J., Kindsvogel W., Jaspers S.,
 RA Chen Z., Dillon S.R., Gao Z., Gilbert T., Madden K., Schlutsmeyer S.,
 RA Yao L., Whitmore T.E., Chandrasekhar Y., Grant F.J., Maurer M.,
 RA Jelinek L., Storey H., Brendler T., Hammond A., Topouzis S.,
 RA Clegg C.H., Foster D.C.;
 RT "A soluble class II cytokine receptor, IL-22RA2, is a naturally
 RT occurring IL-22 antagonist.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9511-9516(2001).
 RN [5]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).

RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.P., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seehagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R.L., Watanabe C., Wileand D., Woods K., Xie M.-H.,
 RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
 RA Wood W.I., Godowski P.J., Gray A.M.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 RN [6]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS PRO-16 AND LYS-190.
 RA Rieder M.J., Johanson E.J., da Ponte S.H., Hastings N.C., Ahearn M.O.,
 RA Bertucci C.B., Wong M.W., Yi Q., Nickerson D.A.;
 RT "SeattleSNPs, NHLBI HL66682 program for genomic applications, UW-
 RT FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
 RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX MEDLINE=22935763; PubMed=14574404; DOI=10.1038/nature02055;
 RA Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,
 RA Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,
 RA Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainscough R.,
 RA Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,
 RA Babbage A.K., Bagguley C.L., Bailey J., Banerjee R., Barker D.J.,
 RA Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,
 RA Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown J.Y.,
 RA Burford D.C., Burrill W., Burton J., Carder C., Carter N.P.,
 RA Chapman J.C., Clark S.Y., Clark G., Clee C.M., Clegg S., Cobley V.,
 RA Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J.,
 RA Culley K.M., Dhani P., Davies J., Dunn M., Earthrowl M.E.,
 RA Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,
 RA Frankland J., French L., Garner P., Garnett J., Ghori M.J.,
 RA Gibby L.M., Gillson C.J., Glithero R.J., Grafham D.V., Grant M.,
 RA Griddle S., Griffiths C., Griffiths M.N.D., Hall R., Halls K.S.,
 RA Hammond S., Harley J.D., Hart E.A., Heath P.D., Heathcote R.,
 RA Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,
 RA Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,
 RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,
 RA Lawlor S., Leongamrert D.A., Leversha M., Lloyd C.R., Lloyd D.M.,
 RA Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi M.,
 RA Maslen G.L., Matthews L., McCann O.T., McLaren S.J., McLay K.,
 RA McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T.,
 RA Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Patel R.,
 RA Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S., Plumb R.W.,
 RA Porter K.M., Ramsey Y., Ranby S.A., Rice C.M., Ross M.T., Searle S.M.,
 RA Sahra H.K., Sheridan E., Skuce C.D., Smith S., Smith M., Spraggon L.,
 RA Squares S.L., Steward C.A., Sycamore N., Tamlyn-Hall G., Tester J.,
 RA Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B.,
 RA Wall M., Wallis J.M., West A.P., White S.S., Whitehead S.L.,
 RA Whittaker H., Wild A., Willey D.J., Wilmer T.E., Wood J.M., Wray P.W.,
 RA Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,
 RA Durbin R., Hubbard T., Sulston J.E., Dunham I., Rogers J., Beck S.;
 RT "The DNA sequence and analysis of human chromosome 6.";
 RL Nature 425:805-811(2003).
 RN [8]
 RP PROTEIN SEQUENCE OF 22-36.
 RX PubMed=15340161; DOI=10.1110/ps.04682504;
 RA Zhang Z., Henzel W.J.;
 RT "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites.";
 RL Protein Sci. 13:2819-2824(2004).
 RN [9]
 RP TISSUE SPECIFICITY.
 RX PubMed=15201862; DOI=10.1038/sj.gene.6364104;
 RA Weiss B., Wolk K., Gruenberg B.H., Volk H.D., Sterry W., Asadullah K.,
 RA Sabat R.;
 RT "Cloning of murine IL-22 receptor alpha 2 and comparison with its
 RT human counterpart.";

Db 64 NFNNVT--TNLNVTECDVSS-LSVY-GAYVLRVTRTEWDESHSDWAVV-RFKPMADTVIGP 118
 QY 140 PEVALTTDEKISVLTAP-----EKWKNRPEDLPVSMQOYISNLKYNVSVLNTKSNRT 193
 Db 119 PSYNVKSSEGTLDVDFGPAADREHDKW-----SLKQYYSWIYRILYWKKGSKK 169
 QY 194 WSQCVTNH--TLVLTWLEPNTLYCVHVESFVPGPRRAQPEKOCARTLKDOSSEFAKII 252
 Db 170 VIHDTKHNEIISQLSEPTIYCIQVGVIPENWKTGERSQELCEQTHNGVTP----- 223
 QY 253 FWYVLPISITVFLSVNG-----YSYRYIHVGKEKH-----PANILIIY 292
 Db 224 VWIV-----VTLLGSLAVIISVPVCFPAFWLYRP-----TKHVFPPSYIFPOHL----- 270
 QY 293 GNEFDKRFVPA---EKVINPFTLISDDSKISHQDMSLLGKSSDVSSLNDPQ---PSG 346
 Db 271 -----KEFFSPVQEEHFFHDLTV-ISEEPK-SQRDETVEEASRTAEHHQDSKQBIIDS 323
 QY 347 NLRPPOBEEE 356
 Db 324 EILPFLERDQ 333

RESULT 11
 I22RA_MOUSE
 ID I22RA_MOUSE STANDARD; PRT; 230 AA.
 AC Q80XF5; Q7TNIS;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Interleukin-22 receptor alpha-2 chain precursor (IL-22R-alpha-2)
 DE (Interleukin 22-binding protein) (IL22BP) (Cytokine receptor family type 2, soluble 1) (CRF2-S1).
 DE Name:IL22ra2;
 GN Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, AND SUBCELLULAR LOCATION.
 RC STRAIN=BALB/c;
 RX MEDLINE=22586333; PubMed=12700595; DOI=10.1038/sj.gene.6363947;
 RA Wei C.-C., Ho T.-W., Liang W.-G., Chen G.-Y., Chang M.-S.;
 RL "Cloning and characterization of mouse IL-22 binding protein."; Genes Immun. 4:204-211(2003).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [MRNA], AND TISSUE SPECIFICITY.
 RC STRAIN=BALB/c; TISSUE=Spleen;
 RX PubMed=15201862; DOI=10.1038/sj.gene.6364104;
 RA Weiss B., Wolk K., Gruenberg B.H., Volk H.D., Sterry W., Aseadullah K., Sabat R.;
 RT "Cloning of murine IL-22 receptor alpha 2 and comparison with its human counterpart";
 RL Genes Immun. 5:330-336(2004).
 CC -1- FUNCTION: Receptor for IL-22. Binds to IL-22, prevents interaction with the functional IL-22R complex and blocks the activity of IL-22 (in vitro). May play an important role as an IL-22 antagonist in the regulation of inflammatory responses.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Highly expressed in lymph nodes and at lower levels in lung, spleen, and thymus. Not expressed in kidney, liver and heart.
 CC -1- SIMILARITY: Belongs to the type II cytokine receptor family.
 CC -1- SIMILARITY: Contains 2 fibronectin type-III domains.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 CC EMBL; AF493604; AAP13730.1; -; mRNA.

DR HSSP; AJ555484; CAD88474.1; -; mRNA.
 DR HSSP; P13726; IJPS.
 DR Ensembl; ENSMUSG00000039760; Mus musculus.
 DR MGI; MGI:2665114; I122ra2.
 DR GO; GO:0005829; C:cytosol; IDA.
 DR GO; GO:0005515; P:protein binding; IPI.
 DR GO; GO:0042516; P:regulation of tyrosine phosphorylation of S...; IDA.
 DR InterPro; IPR000282; Cytok receptor_2.
 DR InterPro; IPR003961; FN_III.
 DR PROSITE; PS0853; FN3; FALSE_NEG.
 KW Receptor; Repeat; Signal.
 FT SIGNAL 1 20 By similarity.
 FT CHAIN 21 230 Interleukin-22 receptor alpha-2 chain.
 FT DOMAIN 30 128 Fibronectin type-III 1.
 FT DOMAIN 129 230 Fibronectin type-III 2.
 FT DISULFID 205 226 By similarity.
 FT CONFLICT 149 149 D -> E (in Ref. 2).
 FT CONFLICT 228 228 Q -> H (in Ref. 2).
 SQ SEQUENCE 230 AA; 26589 MW; 9AEA29768A756A75 CRC64;

Query Match 9.3%; Score 275; DB 1; Length 230;
 Best Local Similarity 31.7%; Pred. No. 4.9e-11;
 Matches 64; Conservative 32; Mismatches 100; Indels 6; Gaps 3;

QY 40 PANITELSNMKNVLQWTPPEGLQGVKVTYVQYFYGQKKWLNKSECRNINRYCDLSA 99
 Db 30 PQKVRFSQSRNFHILHWQAGSSLPNNISYFVQYKYGQSKWEDKVCWCTTALFCDLTN 89
 QY 100 ETSYDEHYQYAKAIWGTGKCSKWAESGRFPFLETQIGPPEVALTTDEKISVLTAP 159
 Db 90 ETLLDPVELYVGRVMTACAGHSASWTPTPTPWETKLDPPVVTITRVNASLRLVLRPPD 149
 QY 160 KWKRPEDLPVSMQOYISNLKYNVSVLNT---KSNRTWSQCVTNHILVLTWLEPNTLYCV 216
 Db 150 LPNRNOSGKNASMETYY-GLVYRVFTINNSLEKEQKAYEG--TQRAVEIRGLPHSSYCV 205
 QY 217 HVESFVPGPRRAQPEKOCAR 238
 Db 207 VAEYQPMFDRSPRSKRCVCV 228

RESULT 12
 IL10R2_MOUSE
 ID IL10R2_MOUSE STANDARD; PRT; 349 AA.
 AC Q61190;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Interleukin-10 receptor beta chain precursor (IL-10R-B) (IL-10R2)
 DE (Cytokine receptor family 2 member 4) (Cytokine receptor class-II, member 4) (CRF2-4).
 GN Names=Il10rb; Synonyms=Crfb4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=97199375; PubMed=9047351; DOI=10.1016/S0378-1119(96)00690-7;
 RA Gibbs V.C., Pennica D.;
 RT "CRF2-4: isolation of cDNA clones encoding the human and mouse proteins";
 RL Gene 186:97-101(1997).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=98130620; PubMed=9463407; DOI=10.1084/jem.187.4.571;
 RA Spencer S.D., Di Marco F., Hootley J., Pitts-Week S., Bauer M., Ryan A.M., Sordal B., Gibbs V.C., Aguet M.;
 RT "The orphan receptor CRF2-4 is an essential subunit of the interleukin 10 receptor";
 RL J. Exp. Med. 187:571-578(1998).
 CC -1- FUNCTION: Receptor for IL10 and IL22. Serves as an accessory chain

```
CC essential for the active IL10 receptor complex and to initiate
CC IL10-induced signal transduction events.
CC -l- SUBCELLULAR LOCATION: Type I membrane protein.
CC -l- SIMILARITY: Belongs to the type II cytokine receptor family.
CC -l- SIMILARITY: Contains 2 fibronectin type-III domains.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U53696; AAC3062.1; -; mRNA.
CC Ensembl; ENSMUSG00000022969; Mus musculus.
CC MGI; MGI:109380; Il10rb.
CC DR GO; GO:0004920; F:interleukin-10 receptor activity; IMP.
CC DR GO; GO:0005515; F:protein binding; IPI.
CC DR InterPro; IPR000282; Cytok_receptor_2.
CC DR InterPro; IPR003961; FN_III.
CC DR PRINTS; PR00346; TISSUEFACTOR.
CC DR PROSITE; PS50853; FN3; 2.
CC DR Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
CC KW SIGNAL 1 19 Potential.
CC FT CHAIN 20 349 Interleukin-10 receptor beta chain.
CC FT TOPO_DOM 20 220 Extracellular (Potential).
CC FT TRANSMEM 221 241 Potential.
CC FT TOPO_DOM 242 349 Cytoplasmic (Potential).
CC FT DOMAIN 22 107 Fibronectin type-III 1.
CC FT DOMAIN 111 208 Fibronectin type-III 2.
CC FT CARBOHYD 49 49 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 102 102 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 161 161 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 199 199 N-linked (GlcNAc...) (Potential).
CC FT DISULFID 66 74 By similarity.
CC FT DISULFID 188 209 By similarity.
CC SQ SEQUENCE 349 AA; 39774 MW; 58BA4F6B86330A39 CRC64;

Query Match 9.1%; Score 267.5; DB 1; Length 349;
Best Local Similarity 27.3%; Pred. No. 3e-10;
Matches 98; Conservative 53; Mismatches 157; Indels 51; Gaps 15;

QY 31 PCVSGGL-----PKPNITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYQG 78
Db 3 PCVAGLGGFLVLPALGMIPPPPEKVRMNSVFNKILQWEP-APPKTNLTFTAQYESYRS 61
QY 79 KKWLNKSECRNIRTYCDLSAETSDEHYQYAKVKAIWGTCSKWAESGRFPFLEQTQIG 138
Db 62 ----FQDHCKRTASTQCDFS-HLSKY-GDYTVRVRAELADEHSEWV-NVTFPCPVEDTIIG 114
QY 139 PPEVALTTDEKTSVLTAPKWKRNPEDLPVSMQOIYSNLKYNVSVLNTKSNRTWSQCV 198
Db 115 PPEMQTESLAESLHLSRFSAPQ-IENEPETW--TLKNIYDSWAYRVQWKNGTNEKFPQVVS 171
QY 199 TNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKOCARTLKQDQSEFKAKIIFWVVL 258
Db 172 PYDSEVLRLNLEPWTTCIQVQGLLDQNRGTGESEPICERTGND---EITPSWIVAILI 228
QY 259 ISITVFLFSVMGYSIYRIHVHGEKH-----PANLIIYGNFDPKRF----FVPAEK 306
Db 229 VSVLVVFLFGCFVVLIIYKTKHTFRSGTSLPQHLKEFLGHPHHSTFLFPFPPEP 288
QY 307 IVINFTITANI---SDDSKISHODMSLLGKSSDVS-----SLNDPQSGNLRPPQEEEV 357
Db 289 AEV-FDKLSIISESGSKQSPEDNCASBPSPDGPPELESKDEAPS-----PPHDDPKL 342

RESULT 13
Q8VHM7_MOUSE
ID Q8VHM7_MOUSE PRELIMINARY; PRT; 351 AA.
AC Q8VHM7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
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DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin 10 receptor 2 precursor.
GN Names=Il10rb; Synonyms=Il10r2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Hardy M.P.; Hertzog P.J.; Omczarek C.M.;
RT "The genomic structure and expression patterns of the gene encoding
RL the second chain of the murine interleukin 10 receptor, IL-10R2."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF440787; AAL40946.1; -; mRNA.
DR PIR; JC6311; JC6311.
DR Ensembl; ENSMUSG00000022969; Mus musculus.
DR MGI; MGI:109380; Il10rb.
DR GO; GO:0004920; F:interleukin-10 receptor activity; IMP.
DR GO; GO:0005515; F:protein binding; IPI.
DR InterPro; IPR000282; Cytok_receptor_2.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR001187; Tissue_factor.
DR PRINTS; PR00346; TISSUEFACTOR.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS50853; FN3; 2.
KW Receptor; Signal; Transmembrane.
FT SIGNAL 1 22 Potential.
FT SEQUENCE 351 AA; 40031 MW; 53102D95809AF5D0 CRC64;

Query Match 8.9%; Score 261; DB 2; Length 351;
Best Local Similarity 27.6%; Pred. No. 8.6e-10;
Matches 96; Conservative 54; Mismatches 158; Indels 40; Gaps 15;

QY 30 VPCVSGGLPKPNITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYQKKNLKNKSECRN 89
Db 17 VPAL-GMIPPPPEKVRMNSVFNKILQWEP-APPKTNLTFTAQYESYRS----FQDHCKR 70
QY 90 INRTYCDLSAETSDEHYQYAKVKAIWGTCSKWAESGRFPFLEQTQIGPPEVALTTDEK 149
Db 71 TASTQCDFS-HLSKY-GDYTVRVRAELADEHSEWV-NVTFPCPVEDTIIGPEMQIESLA 127
QY 150 SISVLTAPKWKRNPEDLPVSMQOIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLE 209
Db 128 SLHLRFSAPQ-IENEPETW--TLKNIYDSWAYRVQWKNGTNEKFKQVSPYDSEVLRLNLE 184
QY 210 PNTLYCVHVESFVPGPPRAQPSKOCARTLKQDQSEFKAKIIFWVVLPISTVFLFSVM 269
Db 185 PWTTCIQVQGLLDQNRGTGESEPICERTGND---EITPSWIVAILIIVSVLWVFLFL 241
QY 270 GYSIYRIHVHGEKH-----PANLIIYGNFDPKRF----FVPAEKIVINFTITANI- 316
Db 242 GCFVVLWLIYKTKHTFRSGTSLPQHLKEFLGHPHHSTFLFPFPPEAEV-FDKLSII 300
QY 317 ---SDDSKISHODMSLLGKSSDVS-----SLNDPQSGNLRPPQEEEV 357
Db 301 SESESGSKQSPEDNCASBPSPDGPPELESKDEAPS-----PPHDDPKL 344

RESULT 14
Q8N6P7_HUMAN
ID Q8N6P7_HUMAN PRELIMINARY; PRT; 574 AA.
AC Q8N6P7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Interleukin 22 receptor, alpha 1.
GN Name=IL22RA1; ORFNames=RP11-293P20.5-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
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OX NCBI_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Adrenal cortex;
RX MDLJNBE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Harte S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Adrenal cortex;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
[3]
RP NUCLEOTIDE SEQUENCE.
RA Chapman J.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
[4]
RP NUCLEOTIDE SEQUENCE.
RA Lad H.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029273; AAH29273.1; -; mRNA.
DR EMBL; AL590683; CAH70116.1; -; Genomic DNA.
DR EMBL; AL591178; CAH72088.1; -; Genomic DNA.
DR EMBL; AL591178; CAH70116.1; JOINED; Genomic DNA.
DR EMBL; AL590683; CAH72088.1; JOINED; Genomic DNA.
DR HSSP; PI3726; ITHF.
DR Ensemble; ENSG00000142677; Homo sapiens.
DR HGNC; HGNC:13700; IL22RA1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000282; Cytok_receptor_2.
DR ProSite; PS50853; FN3; I.
DR Receptor; Repeat; Transmembrane.
SQ SEQUENCE 574 AA; 63077 MW; D46CC71D496F3420 CRC64;

Query Match 8.7%; Score 257; DB 2; Length 574;
Best Local Similarity 22.7%; Pred. No. 3.3e-09;
Matches 134; Conservative 93; Mismatches 243; Indels 120; Gaps 28;

QY 42 NITFLSINMKNVLQW-TPPEGLQGVKVTYVQYFIYQCKWLNKSECRNINRYCDLSAE 100
DB 27 HVKFSQSFENILTWDSGPEGTP--DTVYSIEYKTYGERDWVAKGQCRITRKSCLNLTVE 84
QY 101 TSDYEHQYAKVAIKWGTCKSWAESGRFFPFLETOIGPPEVALTIDKESISVVLTAPEK 160
DB 85 TGNLTLYARVTVAVSAGRSATKMTDRFSSLOHTLTKPDVTCISKVRSIQMIV----- 139
QY 161 WKNPNDELPV-----SMQYISNLYKNVSVLNTKSNRTWSQCV--TNHTLVLTWLEP 210
DB 140 ---HPTPTPIRAGDGHRLTLEDIFHDLFYH---LELQVNRVYQMHLLGKGQREYEFGLTP 193
QY 211 NTLVYCHVESFVGPFPRAQPSKQC-ARTLKQDSSEFAKIIFFWVLPISIVTFLPSVM 269

```


GenCore version 5.1.7
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QM protein - protein search, using sw model

Run on: April 5, 2006, 11:29:48 ; Search time 209.295 Seconds

(without alignments)
1160.927 Million cell updates/sec

Title: US-09-745-792a-11

Perfect score: 2947

Sequence: 1 MRAPGRPALRLPLPLLLL.....NETYLMQFMENGLYQWMEN 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2947	100.0	553	2	Aaw79159
2	2947	100.0	553	4	Aab85268 Human IL-
3	2947	100.0	553	4	Aau04058 Human int
4	2947	100.0	553	5	Abg67199 Human int
5	2947	100.0	553	5	Aae23353 Human int
6	2947	100.0	553	6	Abr38943 Human AK1
7	2947	100.0	553	6	Abp70950 Interleuk
8	2947	100.0	553	8	Adj83291 Human int
9	2947	100.0	553	8	Adj75638 Marker ge
10	2947	100.0	553	8	Adn04874 Antipsori
11	2947	100.0	553	9	Adw64528 Human IL-
12	2947	100.0	553	9	Aea50101 Mouse IL-
13	2947	100.0	553	9	Aea50061 Human IL-
14	2947	100.0	553	9	Aea50099 Mouse IL-
15	2947	100.0	553	9	Aea50103 Mouse IL-
16	2947	100.0	553	9	Aea28837 Human/mou
17	2947	100.0	553	9	Aea28841 House mou
18	2947	100.0	553	9	Aea28839 House mou
19	2947	100.0	553	9	Aea28799 Human int
20	2947	100.0	553	6	Abr38947 Human AK1
21	2943	99.9	553	6	Abr38946 Human AK1
22	2941	99.8	553	4	Abbl1582 Human cla
23	2941	99.8	553	8	Adm95033 Human int
24	2941	99.8	553	9	Aea00133 Human TAT

25	2941	99.8	553	9	Aea00653	Human TAT
26	2937	99.7	553	6	Abr38948	Human AK1
27	2880	97.7	542	4	Aau12265	Human PRO
28	2880	97.7	542	4	Aau29222	Human PRO
29	2880	97.7	542	6	Abu58598	Human PRO
30	2880	97.7	542	6	Abu88146	Novel hum
31	2880	97.7	542	6	Abu84461	Human sec
32	2880	97.7	542	6	Abr66335	Human sec
33	2880	97.7	542	6	Abr65725	Human sec
34	2880	97.7	542	6	Abu99665	Human sec
35	2880	97.7	542	6	Abu82904	Human PRO
36	2880	97.7	542	6	Abol17709	Novel hum
37	2880	97.7	542	6	Abu90025	Novel hum
38	2880	97.7	542	6	Abr68274	Human sec
39	2880	97.7	542	6	Abu96327	Novel hum
40	2880	97.7	542	6	Abu92758	Human sec
41	2880	97.7	542	6	Abu08835	Human sec
42	2880	97.7	542	6	Abu02887	Human sec
43	2880	97.7	542	6	Abr75041	Human sec
44	2880	97.7	542	6	Abr94803	Human sec
45	2880	97.7	542	6	Abu85776	Human PRO

ALIGNMENTS

RESULT 1
AAW79159
ID AAW79159 standard; protein; 553 AA.
XX
AC AAW79159;
XX
DT 20-NOV-1998 (first entry)
XX
DE Zcytor7 cytokine receptor polypeptide.
XX
KW Zcytor7; cytokine receptor; ligand-binding polypeptide; kidney; pancreas;
KW type 2 cytokine receptor family; CRP2; prostate tissue; nervous tissue;
KW agonist; cell proliferation; cell differentiation; renal disease; human;
KW neural disease; pancreatic disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 30..250
FT /note= "extracellular (ligand-binding) domain; sequence claimed in claim 1"
FT Domain 275..553
FT /note= "intracellular domain"
FT
XX WO9837193-A1.
XX 27-AUG-1998.
XX 18-FEB-1998; 98WO-US003029.
XX 20-FEB-1997; 97US-00803305.
XX 02-OCT-1997; 97US-00943087.
XX (ZYMO) ZYMOGENETICS INC.
XX Lok S, Kho CJ, Jelmborg AC, Adams RL, Whitmore TE, Farrah TM;
XX WPI; 1998-480798/41.
XX N-PSDB; AAV57515.
XX Novel human Zcytor7 DNA encodes a type 2 cytokine receptor - useful for
XX treating renal, neural, pancreatic and prostatic diseases.
XX Claim 1; Page 55-59; 72pp; English.
XX This represents the Zcytor7 cytokine receptor. Zcytor7 is a ligand-
XX binding receptor polypeptide and is a novel member of the type 2 cytokine

CC receptor family (CRF2). An expression vector containing the Zcytor
CC polynucleotide, operably linked to transcription promoter, a sequence
CC encoding a transmembrane and intracellular domain, or both, and a
CC transcriptional terminator can be used to transform host cells for the
CC recombinant production of the polypeptide. The sequences can be used to
CC study the Zcytor7 gene and to isolate ligands binding to it. Zcytor7 is
CC preferentially expressed in the kidney, pancreas, prostate or nervous
CC tissue. Agonists of Zcytor7 can be used to stimulate proliferation and
CC differentiation of cell in these organs. The antagonists and agonists can
CC also be used in the treatment of renal, neural, pancreatic and prostate
CC diseases
XX
SQ Sequence 553 AA;

Query Match 100.0%; Score 2947; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 5.6e-240;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGRPALRPLPPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPE 60
Db 1 MRAPGRPALRPLPPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPE 60
QY 61 GLOGVKVTYVQYFIYGQKKWLNKSECRNINRTYCDLSAETSDEYHGYAKVKAIWGTC 120
Db 61 GLOGVKVTYVQYFIYGQKKWLNKSECRNINRTYCDLSAETSDEYHGYAKVKAIWGTC 120
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Db 121 SKWASGRFYPFLETOIGPPEVALTTDEKSI SVLTAPEKWKENPEDLPVSMQIYSNLK 180
QY 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVGPFRRAQPSKQCARTL 240
Db 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVGPFRRAQPSKQCARTL 240
QY 241 KDQSSBFKAKIIPWYVLPISITVFLFSVMGYSIYRIVHGKEKHPANLILYGNFDPKRF 300
Db 241 KDQSSBFKAKIIPWYVLPISITVFLFSVMGYSIYRIVHGKEKHPANLILYGNFDPKRF 300
QY 301 FVPAEKIVINFITLNI SDQSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEVKHL 360
Db 301 FVPAEKIVINFITLNI SDQSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEVKHL 360
QY 361 GYASHLMEIFCDSEENTEGTSFTQBSLSRTIPDPKTVIEYDVVRTTICAGPEEQELS 420
Db 361 GYASHLMEIFCDSEENTEGTSFTQBSLSRTIPDPKTVIEYDVVRTTICAGPEEQELS 420
QY 421 LQBEVSTQGTLLSQAALAVLGPOTLQYSYTPQLQDLPLAQSHTDSEEGPEEPSTTLV 480
Db 421 LQBEVSTQGTLLSQAALAVLGPOTLQYSYTPQLQDLPLAQSHTDSEEGPEEPSTTLV 480
QY 481 DWDPOQTRLCIPSLSGFDQDSECEPSEGDGLGEEGLSLRYEAPADRPDPGENETYLMO 540
Db 481 DWDPOQTRLCIPSLSGFDQDSECEPSEGDGLGEEGLSLRYEAPADRPDPGENETYLMO 540
QY 541 FMEEWGLYVOMEN 553
Db 541 FMEEWGLYVOMEN 553

RESULT 2
AAB85268
ID AAB85268 standard; protein; 553 AA.
XX
AC AAB85268;
XX
DT 07-SEP-2001 (first entry)
XX
DE Human IL-20 receptor subunit IL-20RA.
XX
KW Interleukin 20; IL-20; IL-20RA; Zcytor7; IL-20RB; DIRS1; immunoglobulin;
KW antiinflammatory; antipsoriatic; antiasthmatic; antibacterial; human;
KW dermatological; antiulcer; antagonist.
XX

OS Homo sapiens.
XX WO200146232-A2.
XX
XX 28-JUN-2001.
XX
XX 22-DEC-2000; 2000WO-US035307.
XX
XX 23-DEC-1999; 99US-00471774.
XX
XX 22-JUN-2000; 2000US-0213416P.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Foster DC, Xu W, Madden KL, Kelly JD, Sprecher CA, Brandt CS;
XX Rixon MW, Presnell SR, Fox BA;
XX WPI; 2001-398320/42.
XX N-PSDB; AAH22815.
XX
XX Isolated interleukin 20 soluble receptor comprising two polypeptide
XX subunits IL-20RA and IL-20RB, useful for down-regulating IL-20 and thus
XX treating inflammatory diseases such as psoriasis.
XX
XX Disclosure; Page 63-65; 119pp; English.
XX
XX The invention relates to an interleukin 20 (IL-20) soluble receptor
XX comprising two polypeptide subunits IL-20RA (formerly known as Zcytor7)
XX and IL-20RB (formerly known as DIRS1). The two subunits are preferably
XX linked together. In one embodiment, one subunit is fused to the constant
XX region of the light chain of an immunoglobulin, and the other subunit is
XX fused to constant region of the heavy chain of an immunoglobulin. The
XX light chain and the heavy chain are connected via a disulphide bond. The
XX soluble receptor can be used to down-regulate IL-20 and thus treat
XX inflammatory diseases such as psoriasis, inflammatory lung injury such as
XX asthma or bronchitis, adult respiratory disease (ARD), septic shock,
XX multiple organ failure, bacterial pneumonia, eczema, atopic and contact
XX dermatitis, and inflammatory bowel disease such as ulcerative colitis and
XX Crohn's disease. The present sequence represents a human IL-20 receptor
XX subunit IL-20RA
XX
XX Sequence 553 AA;

Query Match 100.0%; Score 2947; DB 4; Length 553;
Best Local Similarity 100.0%; Pred. No. 5.6e-240;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGRPALRPLPPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPE 60
Db 1 MRAPGRPALRPLPPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPE 60
QY 61 GLOGVKVTYVQYFIYGQKKWLNKSECRNINRTYCDLSAETSDEYHGYAKVKAIWGTC 120
Db 61 GLOGVKVTYVQYFIYGQKKWLNKSECRNINRTYCDLSAETSDEYHGYAKVKAIWGTC 120
QY 121 SKWASGRFYPFLETOIGPPEVALTTDEKSI SVLTAPEKWKENPEDLPVSMQIYSNLK 180
Db 121 SKWASGRFYPFLETOIGPPEVALTTDEKSI SVLTAPEKWKENPEDLPVSMQIYSNLK 180
QY 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVGPFRRAQPSKQCARTL 240
Db 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVGPFRRAQPSKQCARTL 240
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Db 241 KDQSSBFKAKIIPWYVLPISITVFLFSVMGYSIYRIVHGKEKHPANLILYGNFDPKRF 300
QY 301 FVPAEKIVINFITLNI SDQSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEVKHL 360
Db 301 FVPAEKIVINFITLNI SDQSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEVKHL 360
QY 361 GYASHLMEIFCDSEENTEGTSFTQBSLSRTIPDPKTVIEYDVVRTTICAGPEEQELS 420
Db 361 GYASHLMEIFCDSEENTEGTSFTQBSLSRTIPDPKTVIEYDVVRTTICAGPEEQELS 420

QY 421 LOBEVSTQGTLLSQAALAVLGPTQLOYSYTPQLQDLDPLAQHSTDSERGPEEPSTTLV 480
 DB 421 LOBEVSTQGTLLSQAALAVLGPTQLOYSYTPQLQDLDPLAQHSTDSERGPEEPSTTLV 480
 QY 481 DWDPTQGRLCIPSLSSFDQDSECEPSEGDGLGEGLLSRLYEPAADPRPPGGENETVLMQ 540
 DB 481 DWDPTQGRLCIPSLSSFDQDSECEPSEGDGLGEGLLSRLYEPAADPRPPGGENETVLMQ 540
 QY 541 FMEEWGLYVQMEN 553
 DB 541 FMEEWGLYVQMEN 553
 RESULT 3
 AAU04058
 ID AAU04058 standard; protein; 553 AA.
 AC AAU04058;
 XX
 DT 23-OCT-2001 (first entry)
 DE Human interleukin-20 receptor A, IL-20RA.
 KW Human: interleukin-20 receptor A; IL-20RA; antagonist; psoriasis; eczema;
 KW dermatitis; adult respiratory disease; asthma; bronchitis; pneumonia;
 KW multiple organ failure; inflammatory lung injury; septic shock;
 KW bacterial pneumonia; inflammatory bowel disease; rheumatoid arthritis;
 KW ulcerative colitis; Crohn's disease.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 30..250
 FT /label= Extracellular_domain
 PN WO200146261-A1.
 XX
 PD 28-JUN-2001.
 XX
 PF 22-DEC-2000; 2000WO-US035305.
 XX
 PR 23-DEC-1999; 99US-00470898.
 PR 22-JUN-2000; 2000US-0213341P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Thompson P, Foster DC, Wenfeng X, Madden KL, Kelly JD;
 PI Sprecher CA, Blumberg H, Eagan MA, Jaspers SR, Chandrasekhar JA;
 PI Novak JE;
 XX
 DR WPI; 2001-418045/44.
 DR N-PSDB; AAS07643.
 XX
 PT Treating interleukin-20 induced inflammation in a mammal, such as adult
 PT respiratory disease, eczema, psoriasis, contact dermatitis, multiple
 PT organ failure and septic shock, involves administering IL-20 antagonist.
 PS Disclosure; Page 57-59; 117pp; English.
 XX
 CC The sequence represents the Human interleukin-20 receptor A, IL-20RA. The
 CC invention relates to treating a mammal afflicted with a disease in which
 CC an interleukin-20 (IL-20) polypeptide plays a role, involves
 CC administering antagonist of IL-20 polypeptide to the individual. The
 CC method is useful for treating psoriasis, eczema, atopic dermatitis,
 CC contact dermatitis, adult respiratory disease, asthma, bronchitis and
 CC pneumonia and is also useful for treating multiple organ failure,
 CC inflammatory lung injury, septic shock, bacterial pneumonia, inflammatory
 CC bowel disease, rheumatoid arthritis, ulcerative colitis and Crohn's
 CC disease
 XX
 SQ Sequence 553 AA;

Query Match 100.0%; Score 2947; DB 4; Length 553;
 Best Local Similarity 100.0%; Pred No. 5.6e-240;
 Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRAPGRPALRPLPPELLLLLLAAMPGRAPVPCVSGGLPKPANITFLSINNKNVLTQTPPE 60
 DB 1 MRAPGRPALRPLPPELLLLLLAAMPGRAPVPCVSGGLPKPANITFLSINNKNVLTQTPPE 60
 QY 61 GLQGVKVTYVQYFYIYQKKWLNKSECRNINRTYCDLSAETSDYEHQYAKVAIWTGTC 120
 DB 61 GLQGVKVTYVQYFYIYQKKWLNKSECRNINRTYCDLSAETSDYEHQYAKVAIWTGTC 120
 QY 121 SKWAESGRFYPFLETOIGPPEVALTTDEKSIISVLTAPKWKKNRPEDLPVSMQIYSNLK 180
 DB 121 SKWAESGRFYPFLETOIGPPEVALTTDEKSIISVLTAPKWKKNRPEDLPVSMQIYSNLK 180
 QY 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLPNTLYCVHVESFVPGPPRAQPSKQCARTL 240
 DB 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLPNTLYCVHVESFVPGPPRAQPSKQCARTL 240
 QY 241 KQOSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILYGNEDPKRF 300
 DB 241 KQOSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILYGNEDPKRF 300
 QY 301 FYPAEKIVINFITLNISDDSKISHQDMSLLGKSSDVSSSLNDPOPSGNLRPPQBESEVKHL 360
 DB 301 FYPAEKIVINFITLNISDDSKISHQDMSLLGKSSDVSSSLNDPOPSGNLRPPQBESEVKHL 360
 QY 361 GYASHLMEIFCDSEENTEGETSFTQBSLSRTIPPDKTIVIEYDVRTTDCAGPEQELS 420
 DB 361 GYASHLMEIFCDSEENTEGETSFTQBSLSRTIPPDKTIVIEYDVRTTDCAGPEQELS 420
 QY 421 LOBEVSTQGTLLSQAALAVLGPTQLOYSYTPQLQDLDPLAQHSTDSERGPEEPSTTLV 480
 DB 421 LOBEVSTQGTLLSQAALAVLGPTQLOYSYTPQLQDLDPLAQHSTDSERGPEEPSTTLV 480
 QY 481 DWDPTQGRLCIPSLSSFDQDSECEPSEGDGLGEGLLSRLYEPAADPRPPGGENETVLMQ 540
 DB 481 DWDPTQGRLCIPSLSSFDQDSECEPSEGDGLGEGLLSRLYEPAADPRPPGGENETVLMQ 540
 QY 541 FMEEWGLYVQMEN 553
 DB 541 FMEEWGLYVQMEN 553
 RESULT 4
 ABG67199
 ID ABG67199 standard; protein; 553 AA.
 XX
 AC ABG67199;
 XX
 DT 24-SEP-2002 (first entry)
 XX
 DE Human Interleukin-20 sub-unit IL20RA.
 XX
 KW Inflammation; interleukin-20; IL-20; interleukin-8; IL-8; chemokine;
 KW neutrophil; monocyte; basophil; eosinophil; chemoattractant; psoriasis;
 KW periodontal disease; rheumatoid arthritis; idiopathic pulmonary fibrosis;
 KW angiogenesis-dependent chronic inflammatory condition; lung cancer;
 KW melanoma; inflammatory disease; diabetes; arteriosclerosis; cataract;
 KW reperfusion injury; cancer; meningitis; rheumatic disease; skin disease;
 KW idiopathic pulmonary fibrosis; inflammatory bowel disease; psoriasis;
 KW ulcerative colitis; eczema; atopic dermatitis; contact dermatitis;
 KW inflammatory lung disease; ARD; adult respiratory disease; asthma;
 KW bronchitis; pneumonia.
 XX
 OS Homo sapiens.
 XX
 PN US2002042366-A1.
 XX
 PD 11-APR-2002.
 XX
 PF 22-DEC-2000; 2000US-00746359.

XX 23-DEC-1999; 99US-0171969P.
PR 22-JUN-2000; 2000US-0213341P.
XX (THOM/) THOMPSON P.
PA (FOST/) FOSTER D C.
PA (KUMW/) XU W.
PA (MADD/) MADDEN K L.
PA (KELL/) KELLY J D.
PA (SPRE/) SPRECHER C A.
PA (BLUM/) BLUMBERG H.
PA (EAGA/) EAGAN M A.
PA (JASP/) JASPERS S R.
PA (CHAN/) CHANDRASEKHAR Y A.
PA (NOVA/) NOVAK J E.
XX Thompson P, Foster DC, Xu W, Madden KL, Kelly JD, Sprecher CA;
PI Blumberg H, Eagan MA, Jaspers SR, Chandrasekhar YA, Novak JE;
XX N-PSDB; ABR96176.
DR WPI: 2002-507215/54.
DR N-PSDB; ABR96176.
XX
XX Treating inflammatory skin and lung diseases using antibodies against
PT interleukins (IL)-20 (which indirectly modulates activation of IL-8),
PT useful for treating e.g. psoriasis, asthma and bronchitis.
XX
XX Disclosure; Page 20-21; 68pp; English.
XX
XX The invention describes a method (I) for treating a mammal afflicted with
CC a disease in which an interleukin-20 (IL-20) polypeptide plays a role
CC comprising administering antagonist of the IL-20 polypeptide to the
CC individual. An important cytokine in the inflammatory process is
CC interleukin-8 (IL-8), a chemokine that acts as an agonist for neutrophils
CC via chemotaxis and the release of granule enzymes. IL-8 binds to
CC receptors on neutrophils, monocytes, basophils, and eosinophils. IL-8 is
CC a potent chemoattractant for neutrophils; and the early stages of
CC periodontal disease are characterised by the influx of neutrophils. IL-8
CC is a potent inducer of angiogenesis in several angiogenesis-dependent
CC chronic inflammatory conditions, including rheumatoid arthritis,
CC psoriasis, and idiopathic pulmonary fibrosis. Additionally, IL-8 is an
CC important source of angiogenic activity in human lung cancer. Also, IL-8
CC expression correlates with experimental metastatic activity of some
CC melanoma cell lines. Therefore an effective method to treat inflammatory
CC diseases would be to administer an agent that would inhibit IL-8. It has
CC been shown that IL-20 up-regulates IL-8. Therefore antagonists to IL-20
CC can be used to treat these diseases. The method is used for treating
CC diseases in which the IL-20 polypeptide plays a role e.g. inflammatory
CC diseases including diabetes, arteriosclerosis, cataracts, reperfusion
CC injury, cancer, meningitis, rheumatic diseases, idiopathic pulmonary
CC fibrosis, inflammatory bowel disease (ulcerative colitis), skin disease
CC (psoriasis, eczema, atopic dermatitis and contact dermatitis) or an
CC inflammatory lung disease (adult respiratory disease (ARD), asthma,
CC bronchitis and pneumonia). This sequence represents a human interleukin-
CC 20 (IL-20) polypeptide used in developing the method of the invention
XX
XX Sequence 553 AA;
XX
XX Query Match 100.0%; Score 2947; DB 5; Length 553;
XX Best Local Similarity 100.0%; Pred. No. 5.6e-240;
XX Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX 1 MRAPGRPALRPLPPLLLALLAAGRAVPCVSGGLPKPANITFLINKNVLOWTPPE 60
DB 1 MRAPGRPALRPLPPLLLALLAAGRAVPCVSGGLPKPANITFLINKNVLOWTPPE 60
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DB 61 GLQGVKVTYTVQYFIYGQKWLNKSCRNINRTYCDLSAETSDEHYQYAKVKAIWGTRC 120
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DB 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVGPVPRRAQPSKQKQARTL 240
QY 241 KQOSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILYIGNEFDKRF 300
DB 241 KQOSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILYIGNEFDKRF 300
QY 301 FVPAEKIVINFTLNISDDSKISHQDMSLLGKSSDVSSLNDPOPSGNLRPPQSEEEVKHL 360
DB 301 FVPAEKIVINFTLNISDDSKISHQDMSLLGKSSDVSSLNDPOPSGNLRPPQSEEEVKHL 360
QY 361 GYASHLMEIFCDSEENTEFTSQESLSRTIPPDKTIVIEYDVTRTTDICAGPERQELS 420
DB 361 GYASHLMEIFCDSEENTEFTSQESLSRTIPPDKTIVIEYDVTRTTDICAGPERQELS 420
QY 421 LQEEVSTQGLLESQAALAVLGPQTLOYSYTPOLQDLPLAQHHTSEEGPSEEPSTTLV 480
DB 421 LQEEVSTQGLLESQAALAVLGPQTLOYSYTPOLQDLPLAQHHTSEEGPSEEPSTTLV 480
QY 481 DMDPQTRGLCIPSLSSFDQDSEGCSEPGDGLGEGLLSRLYEPAADPPGGENETYLMQ 540
DB 481 DMDPQTRGLCIPSLSSFDQDSEGCSEPGDGLGEGLLSRLYEPAADPPGGENETYLMQ 540
QY 541 FMEEWGLYVQMEN 553
DB 541 FMEEWGLYVQMEN 553
XX
XX RESULT 5
XX ID AAE23353
XX AAE23353 standard; protein; 553 AA.
XX AC AAE23353;
XX DT 27-AUG-2002 (first entry)
XX DE Human interleukin-20 receptor alpha (IL-20RA) protein.
XX KW Human; interleukin-19; IL-19; interleukin-20 receptor alpha; IL-20RA;
KW interleukin-20 receptor beta; IL-20RB; inflammation; atherosclerosis;
KW diabetes; reperfusion injury; cancer; infectious meningitis; cataract;
KW rheumatoid arthritis; rheumatic fever; systemic lupus erythematosus;
KW antibacterial; cytostatic; dermatological; ophthalmological; vasotropic.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Peptide 1..29 /label= signal_peptide
FT Protein 30..553 /note= "Human mature IL-20RA protein"
XX WO200222153-A2.
XX PN 21-MAR-2002.
XX PD 13-SEP-2001; 2001WO-US028557.
XX PF 15-SEP-2000; 2000US-0233305P.
XX PR (ZYMO) ZYMOGENETICS INC.
XX PA Chandrasekhar YA, Jaspers SR;
XX PI WPI; 2002-425815/45.
XX DR N-PSDB; AAD37554.
XX PT Method of down-regulating IL-19 useful for treating inflammation
PT comprises administration of a polypeptide comprised of the extracellular
PT domain of IL-20RA and IL-20RB.
XX PS Disclosure; Page 45-47; 80pp; English.

The present invention relates to a method of down-regulating interleukin (IL)-19. The method involves administration of a polypeptide comprised of the extracellular domain of interleukin-20 receptor alpha (IL-20RA) and the extracellular domain of interleukin-20 receptor beta (IL-20RB). The IL-20RA and IL-20RB are heterodimeric receptors that bind to both IL-19 and mda7. The method is useful for down-regulating IL-19, useful for the treatment of inflammation e.g., in diabetes, arteriosclerosis, cataracts, reperfusion injury, cancer, infectious meningitis, rheumatoid arthritis, rheumatic fever and systemic lupus erythematosus. The present sequence is human IL-20RA protein
 Sequence 553 AA;

Query Match 100.0%; Score 2947; DB 5; Length 553;
Best Local Similarity 100.0%; Pred. No. 5.6e-240;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRAEGRPALRPLPLPPLLLLLLAAAPWGRAVPCVSGGLPKPANITFLSNMKNVLOWTTPPE	60
Dd	1	MRAEGRPALRPLPLPPLLLLLLAAAPWGRAVPCVSGGLPKPANITFLSNMKNVLOWTTPPE	60
Qy	61	GLOGVKVTYTVQVITYFYGOKKWLNSECRNINRTYCDLSAETSDYEHQYAKVAIWTGKC	120
Dd	61	GLOGVKVTYTVQVITYFYGOKKWLNSECRNINRTYCDLSAETSDYEHQYAKVAIWTGKC	120
Qy	121	SKWAESGRFYPFLETQTIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLK	180
Dd	121	SKWAESGRFYPFLETQTIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLK	180
Qy	181	YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNLTYCVHVSEFVPGPPRAAQSPSEKOCARTL	240
Dd	181	YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNLTYCVHVSEFVPGPPRAAQSPSEKOCARTL	240
Qy	241	KDQSSEPAKAIIFWVLPISITVFLFSVMGYSIYRYIHVGKEKH PANILILIYGNFEFKRF	300
Dd	241	KDQSSEPAKAIIFWVLPISITVFLFSVMGYSIYRYIHVGKEKH PANILILIYGNFEFKRF	300
Qy	301	FVPAEKIVINFITLNI SDDSKI SHQDMSLLGKSSDVSSLNDPQP SGNLRPPQE EEEVKHL	360
Dd	301	FVPAEKIVINFITLNI SDDSKI SHQDMSLLGKSSDVSSLNDPQP SGNLRPPQE EEEVKHL	360
Qy	361	GYASHLMEIFCDSBENTEGTSFTQOESLSRTIPPDKTVIEYDYVRTTDICAGPBEQBLS	420
Dd	361	GYASHLMEIFCDSBENTEGTSFTQOESLSRTIPPDKTVIEYDYVRTTDICAGPBEQBLS	420
Qy	421	LQEBVSTQGTLLESQAALAVLGPTQLQSYTPQLQDLDP LAQHETDSEGPEERBSTTLV	480
Dd	421	LQEBVSTQGTLLESQAALAVLGPTQLQSYTPQLQDLDP LAQHETDSEGPEERBSTTLV	480
Qy	481	DWDPQTGRLCIPSLSSFPDQDSEGCPSBSGDGLGBEGLLSRLYE PAPP RPFGENETYLMQ	540
Dd	481	DWDPQTGRLCIPSLSSFPDQDSEGCPSBSGDGLGBEGLLSRLYE PAPP RPFGENETYLMQ	540
Qy	541	PMEEWGLYVQMEN	553
Dd	541	PMEEWGLYVQMEN	553

RESULT 6	
ABR38943	
ID	ABR38943 standard; protein; 553 AA.
XX	
XX	ABR38943;
XX	
DT	10-MAY-2003 (first entry)
XX	
DE	Human AKI55 receptor alpha subunit # SEQ ID 1.
XX	
KW	AKI55 receptor; cytokine receptor; inflammation; Crohn's disease;
KW	autoimmune disease; multiple sclerosis; rheumatoid arthritis; psoriasis;
KW	asthma; allergy; diabetes mellitus; Sjogren's syndrome;
KW	transplant rejection; angiogenesis; cancer.

XX	Homo sapiens.
OS	
XX	WO2003002717-A2.
PN	
XX	09-JAN-2003.
PD	
XX	27-JUN-2002; 2002WO-US020489.
PF	
XX	28-JUN-2001; 2001US-0302176P.
XX	03-JAN-2002; 2002US-0345690P.
PR	
XX	(SCHE) SCHERING CORP.
PA	(FINK/) FINKENSCHER H.
PA	
XX	Finkenschner H, De Waal Malefyt R, Nagalakshmi ML, Moore K;
XX	
PI	
XX	WPI; 2003-278256/27.
DR	
XX	N-PSDB; ABZ79509.
DR	
XX	
XX	New cells recombinantly altered to express an exogenous AK155 cytokine
PT	receptor, useful for identifying agents for treating AK155-mediated
PT	diseases, e.g. inflammation, angiogenesis or cancer.
PT	
XX	
PS	Claim 2; Page 63; 100pp; English.
PS	
XX	
CC	The present invention relates to a cell recombinantly altered to express
CC	an exogenous AK155 cytokine receptor comprising alpha and beta subunits.
CC	The cytokine receptor, when expressed in Ba/F3 cells, binds to AK155 and
CC	stimulates binding of STAT3 to interferon (IFN) gamma-activated
CC	sequences. The cell is useful in expressing AK155 cytokine receptor which
CC	may be used for identifying therapeutic agents useful for treating AK155-
CC	mediated conditions or diseases, such as inflammation (e.g. Crohn's
CC	disease), autoimmune diseases (e.g. multiple sclerosis, rheumatoid
CC	arthritis, psoriasis, asthma, allergies, diabetes mellitus, Sjogren's
CC	syndrome), transplant rejection, angiogenesis, and cancer. The current
CC	sequence represents the human AK155 receptor alpha subunit
XX	
XX	Sequence 553 AA;
SQ	

		Query Match	100.0.%; Score 2947; DB 6; Length 553;	
		Best Local Similarity	100.0%; Pred. No. 5..6e-240; Indels	0; Gaps
		Matches 553; Conservative	0; Mismatches	0;
Qy	1	MRAPGRPALRPLPPLPLLILLALLAAPNGRAVPCVSGGLPKPANITFTLSINMKNVLQTTPPE	60	
Dd	1	MRAPGRPALRPLPPLPLLILLALLAAPNGRAVPCVSGGLPKPANITFTLSINMKNVLQTTPPE	60	
Qy	61	GLOGVKVTYTVFYIGOKKWLNKSCRNINRYCDLSAETSDEHYHQAIVKAIWGTKC	120	
Dd	61	GLOGVKVTYTVFYIGOKKWLNKSCRNINRYCDLSAETSDEHYHQAIVKAIWGTKC	120	
Qy	121	SWAESGRFPFPLETOIGPPEVALTTDCKSIISVVLTAPEKKKNPEDLPVSMQOIYSNLK	180	
Dd	121	SWAESGRFPFPLETOIGPPEVALTTDCKSIISVVLTAPEKKKNPEDLPVSMQOIYSNLK	180	
Qy	181	YNVSVLNTKSNRTWSQCVTNNHTLVLTWLEBPTLYCVHVSESVFGPPRRAPQSKEQCARTL	240	
Dd	181	YNVSVLNTKSNRTWSQCVTNNHTLVLTWLEBPTLYCVHVSESVFGPPRRAPQSKEQCARTL	240	
Qy	241	KDOSSFEFKAKIIFWYVLPITSITVFLESVMGYSIYRIYHGVEKHHPANLLILYGNEDFKRF	300	
Dd	241	KDOSSFEFKAKIIFWYVLPITSITVFLESVMGYSIYRIYHGVEKHHPANLLILYGNEDFKRF	300	
Qy	301	FVPAEKIVINFITLNISDDSKISHQDMSLGGKSSDVSSLNDPOPSGNLRPPQEIEEVXHL	360	
Dd	301	FVPAEKIVINFITLNISDDSKISHQDMSLGGKSSDVSSLNDPOPSGNLRPPQEIEEVXHL	360	
Qy	361	GYASHLMWEIFCDSEENTEGSTFTQQEBSLRTIPDPKTVIYEYVDVRTTIDICAGPESEQELS	420	
Dd	361	GYASHLMWEIFCDSEENTEGSTFTQQEBSLRTIPDPKTVIYEYVDVRTTIDICAGPESEQELS	420	
Qy	421	LQBEVSTQGTLRLSQAALAVLGQPOTLIQYSTPOLQLDLPLAQSHTSOEGPEEPSTTLV	480	

Db 421 LQEEVSTQGLLESQAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEPSTTLV 480
QY 481 DWDPTGRLCIPSLSSFDQDSEGCPSGEGGLGEGLLSRLYEHPADPPGNETYLMQ 540
Db 481 DWDPTGRLCIPSLSSFDQDSEGCPSGEGGLGEGLLSRLYEHPADPPGNETYLMQ 540
QY 541 FMEEWGLYVQMEN 553
Db 541 FMEEWGLYVQMEN 553
RESULT 7
ID ABP70950
XX ABP70950 standard; protein; 553 AA.
AC ABP70950;
XX
DT 17-JUL-2003 (first entry)
XX
DE Interleukin-20 receptor 1, IL-20R1.
XX
KW Cytostatic; interleukin-22R1; interleukin-20R2; Mob-5; interleukin-24;
KW interleukin-20R1; IL-22R1; IL-20R2; IL-24; IL-20R1; cancer.
XX
OS Unidentified.
XX
FN WO2003029262-A2.
XX
PD 10-APR-2003.
XX
PF 29-AUG-2002; 2002WO-US028050.
XX
PR 29-AUG-2001; 2001US-0315684P.
XX
PA (UYVA-) UNIV VANDERBILT.
XX
PI Liang P;
XX
DR WPI; 2003-381601/36.
DR N-PSDB; ACC42677.
XX
XX New complexes of Mob-5 (IL-24) receptors, useful for detecting the
PT presence of cancer (e.g. colorectal cancer) in a patient, particularly as
PT markers for the early diagnosis of cancer, or for screening anti-cancer
PT agents.
XX
PS Disclosure; Page 74-75; 76pp; English.
XX
CC The present invention relates to novel compositions comprising complexes
CC between: (a) interleukin (IL)-22R1 and IL-20R2; (b) Mob-5 (IL-24) and IL-
CC 22R1 and IL-20R2; (c) Mob-5 and IL-20R1 and IL-20R2; (d) Mob-5 and IL-
CC 22R1; (e) Mob-5 and IL-20R2; or (f) Mob-5 and IL-20R1. The compositions
CC are useful for detecting the presence of cancer (e.g. a ras-induced
CC cancer or a colorectal cancer) in a patient. The present sequence is IL-
CC 20R1, used in the compositions of the invention
XX
SQ Sequence 553 AA;
Query Match 100.0%; Score 2947; DB 6; Length 553;
Best Local Similarity 100.0%; Pred. No. 5,6e-240;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRAPGRPALRPLPLPPLLLLLLAAPMGRAVPCVSGGLPKPANITFLSINMKNVLTWTPPE 60
Db 1 MRAPGRPALRPLPLPPLLLLLLAAPMGRAVPCVSGGLPKPANITFLSINMKNVLTWTPPE 60
QY 61 GLOGVKVTVTVQVFIYGQKWLKNSCRNINRNYCDLSAETSDYEHQYAKVAIWGTC 120
Db 61 GLOGVKVTVTVQVFIYGQKWLKNSCRNINRNYCDLSAETSDYEHQYAKVAIWGTC 120
QY 121 SKWABSGRFPFLEQTQIGPPEVALTTDEKSI SVLTAPEKWKRNPDLPVSMQOIYSNLK 180

Db 121 SKWABSGRFPFLEQTQIGPPEVALTTDEKSI SVLTAPEKWKRNPDLPVSMQOIYSNLK 180
QY 181 YNVSVLNTKSNKTWSQCVTNHTLVLTLWLEPNTLYCVHVESFVPGPPRRAPQSEKQCARTL 240
Db 181 YNVSVLNTKSNKTWSQCVTNHTLVLTLWLEPNTLYCVHVESFVPGPPRRAPQSEKQCARTL 240
QY 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHYGKEKHPANLILIYGNEDFKRF 300
Db 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHYGKEKHPANLILIYGNEDFKRF 300
QY 301 FVPAEKIVINFITLNISSDSKI SHQDMSLLGKSSDVSSLNDPQPSGNLAPPQSEEEVKHL 360
Db 301 FVPAEKIVINFITLNISSDSKI SHQDMSLLGKSSDVSSLNDPQPSGNLAPPQSEEEVKHL 360
QY 361 GYASHLMEIFCDSEENTECTSFTQOESLSRTIPPDKTVIEYEDVTRTTDICAGPEOELS 420
Db 361 GYASHLMEIFCDSEENTECTSFTQOESLSRTIPPDKTVIEYEDVTRTTDICAGPEOELS 420
QY 421 LQEEVSTQGLLESQAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEPSTTLV 480
Db 421 LQEEVSTQGLLESQAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEPSTTLV 480
QY 481 DWDPTGRLCIPSLSSFDQDSEGCPSGEGGLGEGLLSRLYEHPADPPGNETYLMQ 540
Db 481 DWDPTGRLCIPSLSSFDQDSEGCPSGEGGLGEGLLSRLYEHPADPPGNETYLMQ 540
QY 541 FMEEWGLYVQMEN 553
Db 541 FMEEWGLYVQMEN 553
RESULT 8
ADJ83291
ID ADJ83291 standard; protein; 553 AA.
XX
AC ADJ83291;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human interleukin receptor IL-20RA subunit full-length protein.
XX
KW inflammation; single chain antibody; interleukin; IL-20; IL-20RA subunit;
KW IL-20RB subunit; antiinflammatory; dermatological; antipsoriatic;
KW antiarthritic; respiratory; antiasthmatic; antiulcer; antibacterial;
KW immunosuppressive; gastrointestinal; skin; psoriasis; eczema;
KW atopic dermatitis; contact dermatitis; lung;
KW adult respiratory distress syndrome; asthma; bronchitis; pneumonia;
KW arthritis; septic shock; multiple organ failure; bowel;
KW ulcerative colitis; Crohn's disease; human; receptor.
XX
OS Homo sapiens.
XX
SN US2004005320-A1.
PN
PD 08-JAN-2004.
XX
PF 28-APR-2003; 2003US-00424658.
XX
PR 23-DEC-1999; 99US-0171969P.
PR 22-JUN-2000; 2000US-0213341P.
PR 22-DEC-2000; 2000US-00746359.
XX
XX (THOM/) THOMPSON P.
PA (FOST/) FOSTER D C.
PA (XUWW/) XU W.
PA (MADD/) MADDEN K L.
PA (KELL/) KELLY J D.
PA (SPRE/) SPRECHER C A.
PA (BLUM/) BLUMBERG H.
PA (EAGA/) EAGAN M A.
PA (JASP/) JASPERS S R.
PA (CHAN/) CHANDRASEKHER Y A.
PA (NOVA/) NOVAK J E.

XX Thompson P, Foster DC, Xu W, Madden KL, Kelly JD, Sprecher CA;
PI Blumberg H, Bagan MA, Jaspers SR, Chandrasekhar YA, Novak JE;
XX WPI; 2004-081696/08.
XX N-PSDB; ADJ83290.
XX Reducing or treating inflammation, e.g. inflammatory lung disease,
PT comprises administering an antibody, antibody fragment or single chain
PT antibody that specifically binds to an interleukin (IL)-20RA subunit of
PT an IL-20 receptor.
XX
XX Example 5; SEQ ID NO 11; 69pp; English.
XX
XX The invention relates to a novel method of reducing or treating
CC inflammation in a mammal which comprises administering an antibody,
CC antibody fragment or single chain antibody which specifically binds to a
CC receptor of interleukin (IL)-20 comprising an IL-20RA subunit and an IL-
CC 20RB subunit. The method of the invention has antiinflammatory,
CC dermatological, antipruritic, antiarthritic, respiratory, antiasthmatic,
CC antitumor, antibacterial, immunosuppressive and gastrointestinal
CC applications and may be useful for reducing or treating an inflammation,
CC including an inflammatory skin disease such as psoriasis, eczema, atopic
CC dermatitis and contact dermatitis or an inflammatory lung disease such as
CC adult respiratory distress syndrome, asthma, bronchitis and pneumonia, as
CC well as arthritis, septic shock, multiple organ failure, inflammatory
CC bowel disease, ulcerative colitis or Crohn's disease. The current
CC sequence is that of the human IL-20RA subunit-related protein of the
CC invention.
XX
XX Sequence 553 AA;
SQ

Query Match 100.0%; Score 2947; DB 8; Length 553;
Best Local Similarity 100.0%; Pred. No. 5.6e-240;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPGRPALRPLPPLLLILLALPACRAVPCVSGGLPKPANITFLSINKNVLTQTPPE 60
Db 1 MRAPGRPALRPLPPLLLILLALPACRAVPCVSGGLPKPANITFLSINKNVLTQTPPE 60

Qy 61 GLOGVKTYYTVQVFIYQKQKWLKNSCRNINRYCDLSAETSDYEHQYAKVAIWGTC 120
Db 61 GLOGVKTYYTVQVFIYQKQKWLKNSCRNINRYCDLSAETSDYEHQYAKVAIWGTC 120

Qy 121 SKWAESGRFPFLETQIGPPEVALTTDEKSIISVLTAPKWKKNPBDLPVSMQOIYVSNLK 180
Db 121 SKWAESGRFPFLETQIGPPEVALTTDEKSIISVLTAPKWKKNPBDLPVSMQOIYVSNLK 180

Qy 181 YNVSVLNTKSNRTWSQCVNHTLVLTWLEPNTLYCVHVESFVGPFPRAQPSKQCARTL 240
Db 181 YNVSVLNTKSNRTWSQCVNHTLVLTWLEPNTLYCVHVESFVGPFPRAQPSKQCARTL 240

Qy 241 KDQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILYGNFDPKRF 300
Db 241 KDQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILYGNFDPKRF 300

Qy 301 FVPAEKIVINFITINISDDSKI SHQDMSLLGKSSDVSSSLNDPQPSGNLRPPQEEEVGHL 360
Db 301 FVPAEKIVINFITINISDDSKI SHQDMSLLGKSSDVSSSLNDPQPSGNLRPPQEEEVGHL 360

Qy 361 GYASHLMEIFCDSEENTGTSFTQSSLSRTIPDKTVIIEYDVRTTDCAGPESQELS 420
Db 361 GYASHLMEIFCDSEENTGTSFTQSSLSRTIPDKTVIIEYDVRTTDCAGPESQELS 420

Qy 421 LOSEVSTQGLTLLSQALAVLGQTLQYSYTPQLQDLPLAQSHHTDSEGPPEPSTTLV 480
Db 421 LOSEVSTQGLTLLSQALAVLGQTLQYSYTPQLQDLPLAQSHHTDSEGPPEPSTTLV 480

Qy 481 DWDPTQGRLCIPSLSSFDQSEGCSESGDGLGEGLLSLRYEAPAPDRPPGNETYLMQ 540
Db 481 DWDPTQGRLCIPSLSSFDQSEGCSESGDGLGEGLLSLRYEAPAPDRPPGNETYLMQ 540

Qy 541 FMEEWGLYVQMEN 553

Db 541 FMEEWGLYVQMEN 553
|||||
RESULT 9
ADJ75638
XX ADJ75638 standard; protein; 553 AA.
XX ADJ75638;
XX 20-MAY-2004 (first entry)
XX Marker gene related amino acid sequence SEQ ID NO:890.
XX
XX bronchial asthma; chronic obstructive pulmonary disease;
KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
KW gene therapy; marker.
XX Homo sapiens.
XX EP1394274-A2.
XX 03-MAR-2004.
XX 04-AUG-2003; 2003EP-00254857.
XX 06-AUG-2002; 2002JP-00229312.
PR 20-MAR-2003; 2003JP-00077212.
XX
XX (GENO-) GENOX RES INC.
XX
XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;
PI WPI; 2004-193155/19.
XX
XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
PT comparing the expression level of a marker gene in a biological sample
PT from a subject with the expression level of the gene in a sample from a
PT healthy subject.
XX
XX Example 11; SEQ ID NO 890; 241pp; English.
XX
XX The present invention describes a method of testing for bronchial asthma
CC or chronic obstructive pulmonary disease. The method comprises
CC determining the expression level of a marker gene in a biological sample
CC from a subject, comparing the expression level determined with the
CC expression level of the marker gene in a biological sample from a healthy
CC subject, and judging whether the subject has bronchial asthma or chronic
CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
CC genes (S1) whose expression levels increase when respiratory epithelial
CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
CC whose expression levels decrease when respiratory epithelial cells are
CC stimulated with interleukin-13. Also described: (1) a reagent (I) for
CC testing for bronchial asthma or chronic obstructive pulmonary disease;
CC (2) a kit for screening for a candidate compound for a therapeutic agent
CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
CC an animal model for bronchial asthma or chronic obstructive pulmonary
CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
CC method for producing an animal model for bronchial asthma or chronic
CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
CC asthma or chronic obstructive pulmonary disease, comprising the compound,
CC a marker gene or an antisense nucleic acid corresponding to a portion of
CC the marker gene, a ribozyme, a polynucleotide that suppresses the
CC expression of the gene through an RNAi effect or an antibody recognizing
CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
CC probe has been immobilised to assay a marker gene. (I) has respiratory
CC and antiasthmatic activities, and can be used in gene therapy. The method
CC is useful for testing for or screening for a therapeutic agent for
CC bronchial asthma or chronic obstructive pulmonary disease. The present
CC sequence is used in the exemplification of the present invention.
XX
XX Sequence 553 AA;

Query Match 100.0%; Score 2947; DB 8; Length 553;
Best Local Similarity 100.0%; Pred. No. 5.6e-240;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGRPALRPLPPLPPLLLLLAAPWGRAVPVCVSGGLPKPANITFLSINNKNVLTWTPPE 60
DB 1 MRAPGRPALRPLPPLPPLLLLLAAPWGRAVPVCVSGGLPKPANITFLSINNKNVLTWTPPE 60

QY 61 GLQGVKVTYVQVFIYGQKWLKNSCRNINRYCDLSAETSDYEHQYAKVKAIWGTC 120
DB 61 GLQGVKVTYVQVFIYGQKWLKNSCRNINRYCDLSAETSDYEHQYAKVKAIWGTC 120

QY 121 SKWASGRFPFLETQIGPPEVALTTDEKSI SVLTAPEKWKNPEDLPVSMQOIYSNLK 180
DB 121 SKWASGRFPFLETQIGPPEVALTTDEKSI SVLTAPEKWKNPEDLPVSMQOIYSNLK 180

QY 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQCARTL 240
DB 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQCARTL 240

QY 241 KQOSSSEFKAKIIPWYVLPISITVFLPSVMGYSIYRIVHGKEKHPANLILIIYGNFDFKRF 300
DB 241 KQOSSSEFKAKIIPWYVLPISITVFLPSVMGYSIYRIVHGKEKHPANLILIIYGNFDFKRF 300

QY 301 FVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPOPSGNLRPPQBESEVVKHL 360
DB 301 FVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPOPSGNLRPPQBESEVVKHL 360

QY 361 GVASHLMEIFCDSEENTEGTSFTQESLSRTIPPDKTVIEYDVRTTIDICAGPEEQELS 420
DB 361 GVASHLMEIFCDSEENTEGTSFTQESLSRTIPPDKTVIEYDVRTTIDICAGPEEQELS 420

QY 421 LQBEVSTQGTLLSQALAVLGPQTLOYSYTTPQLQDLPLAQHSTDSEEGPEEPSTTLV 480
DB 421 LQBEVSTQGTLLSQALAVLGPQTLOYSYTTPQLQDLPLAQHSTDSEEGPEEPSTTLV 480

QY 481 DWDPTQGRLCIPSLSSFDQDSECEPSEGDLGEEGLLSRLYEEDPADPPGNETIYLMQ 540
DB 481 DWDPTQGRLCIPSLSSFDQDSECEPSEGDLGEEGLLSRLYEEDPADPPGNETIYLMQ 540

QY 541 FMEEWGLYQMEN 553
DB 541 FMEEWGLYQMEN 553

RESULT 10
ID ADN04874 standard; protein; 553 AA.

XX AC ADN04874;
XX DT 01-JUL-2004 (first entry)
XX DE Antipsoriatic protein sequence #617.
XX KW antipsoriatic; gene therapy; psoriasis; diagnosis.
XX OS Homo sapiens.
XX PN WO2004028479-A2.
XX PD 08-APR-2004.
XX PF 25-SEP-2003; 2003WO-US030907.
XX PR 25-SEP-2002; 2002US-0414006P.
XX PA (GETH) GENENTECH INC.

XX PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
XX PI Wu TD;
XX

DR WPI; 2004-305105/28.
XX N-PSDB; ADN04873.
PT New PRO nucleic acid or polypeptide, useful for preparing a
PT pharmaceutical composition for diagnosing or treating psoriasis in a
XX mammal.
PS Claim 9; SEQ ID NO 1268; 3069pp; English.
XX

CC The invention relates to novel polynucleotide and polypeptides for
CC treating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polypeptides of the invention.
XX
SQ Sequence 553 AA;

Query Match 100.0%; Score 2947; DB 8; Length 553;
Best Local Similarity 100.0%; Pred. No. 5.6e-240;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGRPALRPLPPLPPLLLLLAAPWGRAVPVCVSGGLPKPANITFLSINNKNVLTWTPPE 60
DB 1 MRAPGRPALRPLPPLPPLLLLLAAPWGRAVPVCVSGGLPKPANITFLSINNKNVLTWTPPE 60

QY 61 GLQGVKVTYVQVFIYGQKWLKNSCRNINRYCDLSAETSDYEHQYAKVKAIWGTC 120
DB 61 GLQGVKVTYVQVFIYGQKWLKNSCRNINRYCDLSAETSDYEHQYAKVKAIWGTC 120

QY 121 SKWASGRFPFLETQIGPPEVALTTDEKSI SVLTAPEKWKNPEDLPVSMQOIYSNLK 180
DB 121 SKWASGRFPFLETQIGPPEVALTTDEKSI SVLTAPEKWKNPEDLPVSMQOIYSNLK 180

QY 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQCARTL 240
DB 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQCARTL 240

QY 241 KQOSSSEFKAKIIPWYVLPISITVFLPSVMGYSIYRIVHGKEKHPANLILIIYGNFDFKRF 300
DB 241 KQOSSSEFKAKIIPWYVLPISITVFLPSVMGYSIYRIVHGKEKHPANLILIIYGNFDFKRF 300

QY 301 FVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPOPSGNLRPPQBESEVVKHL 360
DB 301 FVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPOPSGNLRPPQBESEVVKHL 360

QY 361 GVASHLMEIFCDSEENTEGTSFTQESLSRTIPPDKTVIEYDVRTTIDICAGPEEQELS 420
DB 361 GVASHLMEIFCDSEENTEGTSFTQESLSRTIPPDKTVIEYDVRTTIDICAGPEEQELS 420

QY 421 LQBEVSTQGTLLSQALAVLGPQTLOYSYTTPQLQDLPLAQHSTDSEEGPEEPSTTLV 480
DB 421 LQBEVSTQGTLLSQALAVLGPQTLOYSYTTPQLQDLPLAQHSTDSEEGPEEPSTTLV 480

QY 481 DWDPTQGRLCIPSLSSFDQDSECEPSEGDLGEEGLLSRLYEEDPADPPGNETIYLMQ 540
DB 481 DWDPTQGRLCIPSLSSFDQDSECEPSEGDLGEEGLLSRLYEEDPADPPGNETIYLMQ 540

QY 541 FMEEWGLYQMEN 553
DB 541 FMEEWGLYQMEN 553

RESULT 11
ADW64528 standard; protein; 553 AA.

XX AC ADW64528;
XX DT 24-MAR-2005 (first entry)
XX DE Human IL-20RA protein.
XX KW Therapy; cns-gen.; respiratory-gen.; antiasthmatic; antipsoriatic;

KW	antiinflammatory; psoriasis; dermatological disease; immune disorder;	301	FVPAEKIVINFTLNISDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEVKHL	360
KW	pulmonary disease; asthma; inflammation; respiratory disease; bronchitis;	361	GYASHLMEIFCDSEFTECTSTQOBSLSRTIPDQKTVIEYVDVTRTDDICAGPEEOELS	420
KW	antiinflammatory; inflammation; cystic fibrosis;	361	GYASHLMEIFCDSEFTECTSTQOBSLSRTIPDQKTVIEYVDVTRTDDICAGPEEOELS	420
KW	gastrointestinal disease; chemotherapy; interleukin.	421	LOEEVSTQGTLLSQAALAVLGPQTLLQYSYTPQLQDLPLAQEHDTSEEGPEEPSTTLV	480
OS	Homo sapiens.	421	LOEEVSTQGTLLSQAALAVLGPQTLLQYSYTPQLQDLPLAQEHDTSEEGPEEPSTTLV	480
XX	US2005003475-A1.	421	LOEEVSTQGTLLSQAALAVLGPQTLLQYSYTPQLQDLPLAQEHDTSEEGPEEPSTTLV	480
XX	06-JAN-2005.	481	DWDPTQGRICIPSLSSFDQDSECEPSEGGLGEGLLSRLYBEPAPDRPPGNETYLMQ	540
XX	22-DEC-2000; 2000US-00745792.	481	DWDPTQGRICIPSLSSFDQDSECEPSEGGLGEGLLSRLYBEPAPDRPPGNETYLMQ	540
XX	23-DEC-1999; 99US-0171966P.	541	FMEEWGLYQOMEN 553	
XX	22-JUN-2000; 2000US-0213416P.	541	FMEEWGLYQOMEN 553	
XX	(POST/) FOSTER D C.			
PA	(XUMW/) XU W.			
PA	(MADD/) MADDEN K L.			
PA	(KELL/) KELLY J D.			
PA	(SPRE/) SPRECHER C A.			
PA	(BRAN/) BRANDT C S.			
PA	(RIXO/) RIXON M W.			
PA	(PRES/) PRESNELL S R.			
PA	(FOX/) FOX B A.			
XX	Foster DC, Xu W, Madden KL, Kelly JD, Sprecher CA, Brandt CS;			
PI	Rixon MW, Preenell SR, Fox BA;			
XX	WPI; 2005-065240/07.			
DR	N-PSDB; ADW64527.			
XX				
XX	New isolated soluble receptor comprised of an interleukin 20 receptor			
PT	alpha (IL-20RA) subunit and a IL-20RB subunit, useful for treating			
PT	inflammatory diseases e.g., psoriasis and inflammatory lung diseases			
PT	e.g., asthma.			
XX				
PS	Example 5; SEQ ID NO 11; 73pp; English.			
XX				
CC	The present invention relates to a soluble receptor having an			
CC	interleukin 20 receptor alpha (IL-20RA) subunit and an IL-20RB subunit.			
CC	The invention is useful for treating inflammatory diseases such as			
CC	psoriasis and inflammatory lung diseases such as asthma, bronchitis and			
CC	cystic fibrosis. The present sequence is the human IL-20RA protein.			
XX				
SQ	Sequence 553 AA;			
Query Match 100.0%; Score 2947; DB 9; Length 553;				
Best Local Similarity 100.0%; Pred. No. 5.6e-240;				
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 MRAPGRPALRPLPLPPLLLLLAAMPGRAPVPCVSGGLPKPANITPLSNMKNVLTQTPPE	60		
DB	1 MRAPGRPALRPLPLPPLLLLLAAMPGRAPVPCVSGGLPKPANITPLSNMKNVLTQTPPE	60		
QY	61 GLOGVKVTYVQYPIYQCKWLKNSCRNINRYCDLSAETSDYEHQYAKVKAINGTKC	120		
DB	61 GLOGVKVTYVQYPIYQCKWLKNSCRNINRYCDLSAETSDYEHQYAKVKAINGTKC	120		
QY	121 SKWASGRFPYFPLETOIGPPEVALTTDEKSIISVLTAPKWKKNRPEDLPVSMQOIIYSNLK	180		
DB	121 SKWASGRFPYFPLETOIGPPEVALTTDEKSIISVLTAPKWKKNRPEDLPVSMQOIIYSNLK	180		
QY	181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVFGPPRRAPQSEKQCARTL	240		
DB	181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVFGPPRRAPQSEKQCARTL	240		
QY	241 KQSSFEKAKIIPWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILYGNEDFKRP	300		
DB	241 KQSSFEKAKIIPWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILYGNEDFKRP	300		
QY	301 FVPAEKIVINFTLNISDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEVKHL	360		
DB	301 FVPAEKIVINFTLNISDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEVKHL	360		

CC treating a mammal afflicted with an inflammatory disease in which IL-20
CC plays a role such that the inflammation is reduced, where the antagonist
CC comprises an antibody, antibody fragment, or binding polypeptide that
CC specifically binds a polypeptide or polypeptide fragment of IL-20 or a
CC polypeptide or polypeptide fragment of IL-20, and where the inflammatory
CC activity of IL-20 is reduced. The method is useful for producing such
CC therapeutic antibody. The antibody or antibody fragment, produced using
CC the above method, binds to IL-20, and inhibits or reduces the pro-
CC inflammatory activity of IL-20. IL-20-induced proliferation or
CC differentiation of hematopoietic cells and hematopoietic cell progenitors
CC may be reduced or inhibited using the antibody.
XX
SQ Sequence 553 AA;

Query Match 100.0%; Score 2947; DB 9; Length 553;
Best Local Similarity 100.0%; Pred. No. 5.6e-240;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRAPGRPALRPLPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSNKNVLTWTPPE 60
Db 1 MRAPGRPALRPLPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSNKNVLTWTPPE 60
QY 61 GLQGVKVTYVQYFYIGQKKWLKNSCRNINRTYCDLSAETSDYEHQYAKVAIWTGTC 120
Db 61 GLQGVKVTYVQYFYIGQKKWLKNSCRNINRTYCDLSAETSDYEHQYAKVAIWTGTC 120
QY 121 SKWASGRFPFLETOIGPPEVALTTDEKSIISVLTAPKWKKNPDLPSVMOQIYSNLK 180
Db 121 SKWASGRFPFLETOIGPPEVALTTDEKSIISVLTAPKWKKNPDLPSVMOQIYSNLK 180
QY 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVGGPPRRAPQSEKQCARTL 240
Db 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVGGPPRRAPQSEKQCARTL 240
QY 241 KQSSSEFKAKIIPWYVLPISITVFLPSVMGYSIYRIHVGEKHPANLILYGNFDPKRP 300
Db 241 KQSSSEFKAKIIPWYVLPISITVFLPSVMGYSIYRIHVGEKHPANLILYGNFDPKRP 300
QY 301 FYPAEKIVNFITLNTSDSKISHQDMSLLGKSSDVSSLNDPQSGNLRPPQSEEVKHL 360
Db 301 FYPAEKIVNFITLNTSDSKISHQDMSLLGKSSDVSSLNDPQSGNLRPPQSEEVKHL 360
QY 361 GYASHLMEIFCDSEENTEGTSFTQBSLSRTIPPDKTIVIEYDVRTTICAGPEQEELS 420
Db 361 GYASHLMEIFCDSEENTEGTSFTQBSLSRTIPPDKTIVIEYDVRTTICAGPEQEELS 420
QY 421 LQEVSTQGTLLSQALAVLGPQTILQYSVTPQLDPLAQHHTDSBEGPEEPSTTLV 480
Db 421 LQEVSTQGTLLSQALAVLGPQTILQYSVTPQLDPLAQHHTDSBEGPEEPSTTLV 480
QY 481 DMDPQTRGLCIPSLSSFDQDSECEPSEGGDLGEGLLSRLYEAPDRPPGENETYLMO 540
Db 481 DMDPQTRGLCIPSLSSFDQDSECEPSEGGDLGEGLLSRLYEAPDRPPGENETYLMO 540
QY 541 FMEEWGLYQMEN 553
Db 541 FMEEWGLYQMEN 553

RESULT 13
AEA50061
ID AEA50061 standard; protein; 553 AA.
XX
AC AEA50061;
XX
XX 11-AUG-2005 (first entry)
XX Human IL-20RA extracellular domain.
XX Antinflammatory; Gastrointestinal-Gen.; Antiulcer; Antiarthritic;
KW Dermatological; Antipsoriatic; Antibacterial; Immunosuppressive;
KW Antimicrobial; IL-Antagonist-20; Interleukin-20; IL-20; inflammation;
KW inflammatory bowel disease; ulcerative colitis; Crohns disease;

KW arthritis; atopic dermatitis; psoriasis; endotoxemia; septicemia;
KW toxic shock syndrome; infectious disease.
OS Homo sapiens.
XX Synthetic.
XX WO2005052000-A2.
XX 09-JUN-2005.
XX 19-NOV-2004; 2004WO-US039071.
XX 21-NOV-2003; 2003US-0524131P.
PR 24-MAR-2004; 2004US-0555857P.
XX (ZYMO) ZYMOGENETICS INC.
PA
XX Xu W, Kindsvogel WR, Chen Z, Hughes SD, Chandrasekher YA;
PI Dillon SR, Lehner JM, Siadak AW, Sivakumar PV, Moore MD;
XX WPI: 2005-405359/41.
XX N-PSDB; AEA50060.
XX Producing an antibody to an interleukin-20 (IL-20) polypeptide, useful
PT for treating inflammatory diseases e.g., Crohn's disease, by inoculating
PT an animal with the polypeptide eliciting an immune response to produce
XX the antibody.
PS Example 7; SEQ ID NO 14; 2689pp; English.
XX This sequence represents the human interleukin-20RA (IL-20RA)
CC extracellular domain which was used generation of a human IL-20RA
CC extracellular domain immunoglobulin gamma 1 heavy chain constant region
CC fusion construct. The method of the invention for producing an antibody
CC to IL-20 comprises inoculating an animal with an IL-20 polypeptide which
CC elicits an immune response in the animal to produce the antibody, and
CC isolating the antibody from the animal. The antibody is useful for
CC treating a pathological condition in a subject associated with IL-20
CC activity such as chronic inflammatory condition, specifically
CC inflammatory bowel disease, ulcerative colitis, Crohns' disease,
CC arthritis, atopic dermatitis and psoriasis, or acute inflammatory
CC condition such as endotoxemia, septicemia, toxic shock syndrome and
CC infectious disease. An antagonist of IL-20 is useful for treating a
CC mammal afflicted with an inflammatory disease in which IL-20 plays a role
CC such that the inflammation is reduced, where the antagonist comprises an
CC antibody, antibody fragment, or binding polypeptide that specifically
CC binds a polypeptide or polypeptide fragment of IL-20 or a polypeptide or
CC polypeptide fragment of IL-20, and where the inflammatory activity of IL-
CC 20 is reduced. The method is useful for producing such therapeutic
CC antibody. The antibody or antibody fragment, produced using the above
CC method, binds to IL-20, and inhibits or reduces the pro-inflammatory
CC activity of IL-20. IL-20-induced proliferation or differentiation of
CC hematopoietic cells and hematopoietic cell progenitors may be reduced or
CC inhibited using the antibody.
XX
SQ Sequence 553 AA;

Query Match 100.0%; Score 2947; DB 9; Length 553;
Best Local Similarity 100.0%; Pred. No. 5.6e-240;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRAPGRPALRPLPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSNKNVLTWTPPE 60
Db 1 MRAPGRPALRPLPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSNKNVLTWTPPE 60
QY 61 GLQGVKVTYVQYFYIGQKKWLKNSCRNINRTYCDLSAETSDYEHQYAKVAIWTGTC 120
Db 61 GLQGVKVTYVQYFYIGQKKWLKNSCRNINRTYCDLSAETSDYEHQYAKVAIWTGTC 120
QY 121 SKWASGRFPFLETOIGPPEVALTTDEKSIISVLTAPKWKKNPDLPSVMOQIYSNLK 180
Db 121 SKWASGRFPFLETOIGPPEVALTTDEKSIISVLTAPKWKKNPDLPSVMOQIYSNLK 180

QY 181 YNVSVLNKSRTWSQCVTNHTLVLTLWLEPNTLYCVHVESFVPGPPRAQPSKQCARTL 240
 DB 181 YNVSVLNKSRTWSQCVTNHTLVLTLWLEPNTLYCVHVESFVPGPPRAQPSKQCARTL 240
 QY 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILYGNEDKRF 300
 DB 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILYGNEDKRF 300
 QY 301 FVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQBESEVKHL 360
 DB 301 FVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQBESEVKHL 360
 QY 361 GVASHLMEIFCDSEENTEGTSFTQBSLSRTIPDPKTVIEYDVVTTDTCAGPEQELS 420
 DB 361 GVASHLMEIFCDSEENTEGTSFTQBSLSRTIPDPKTVIEYDVVTTDTCAGPEQELS 420
 QY 421 LQEEVSTQGTLLSQALAVLGPQTLYSYTPOQLDPLAQHSDSEEGPEEPSTTLV 480
 DB 421 LQEEVSTQGTLLSQALAVLGPQTLYSYTPOQLDPLAQHSDSEEGPEEPSTTLV 480
 QY 481 DWDPTQGLRCLIPSLSSFDQDSECEPSEGDGLGEGLLSRLYEPAADPPGNETYLMQ 540
 DB 481 DWDPTQGLRCLIPSLSSFDQDSECEPSEGDGLGEGLLSRLYEPAADPPGNETYLMQ 540
 QY 541 FMEEWGLYVQMEN 553
 DB 541 FMEEWGLYVQMEN 553

RESULT 14
 ID AEA50099 standard; protein; 553 AA.
 AC AEA50099;
 DT 11-AUG-2005 (first entry)
 DE Mouse IL-20RA.
 KW Antinflammatory; Gastrointestinal-Gen.; Anticancer; Antiarthritic;
 KW Dermatological; Antiparasitic; Antibacterial; Immunosuppressive;
 KW Antimicrobial; IL-Antagonist-20; interleukin-20; IL-20; inflammation;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 KW arthritis; atopic dermatitis; psoriasis; endotoxemia; septicemia;
 KW toxic shock syndrome; infectious disease; expressed sequence tag.
 OS Mus sp.
 OS Synthetic.
 PN WO2005052000-A2.
 XX 09-JUN-2005.
 XX 19-NOV-2004; 2004WO-US039071.
 XX 21-NOV-2003; 2003US-0524131P.
 XX 24-MAR-2004; 2004US-0555857P.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Xu W, Kindevogel WR, Chen Z, Hughes SD, Chandrasekhar YA;
 PI Dillon SR, Lehner JM, Siadak AW, Sivakumar PV, Moore MD;
 XX WPI: 2005-405359/41.
 DR N-PSDB; AEA50100.
 XX Producing an antibody to an interleukin-20 (IL-20) polypeptide, useful
 PT for treating inflammatory diseases e.g., Crohn's disease, by inoculating
 PT an animal with the polypeptide eliciting an immune response to produce
 PT the antibody.
 XX Example 2; SEQ ID NO 52; 268pp; English.

CC This sequence represents murine interleukin-20RA (IL-20RA). The method of
 CC the invention for producing an antibody to IL-20 comprises inoculating an
 CC animal with an IL-20 polypeptide which elicits an immune response in the
 CC animal to produce the antibody, and isolating the antibody from the
 CC animal. The antibody is useful for treating a pathological condition in a
 CC subject associated with IL-20 activity such as chronic inflammatory
 CC condition, specifically inflammatory bowel disease, ulcerative colitis,
 CC Crohn's disease, arthritis, atopic dermatitis and psoriasis, or acute
 CC inflammatory condition such as endotoxemia, septicemia, toxic shock
 CC syndrome and infectious disease. An antagonist of IL-20 is useful for
 CC treating a mammal afflicted with an inflammatory disease in which IL-20
 CC plays a role such that the inflammation is reduced, where the antagonist
 CC comprises an antibody, antibody fragment, or binding polypeptide that
 CC specifically binds a polypeptide or polypeptide fragment of IL-20 or a
 CC polypeptide or polypeptide fragment of IL-20, and where the inflammatory
 CC activity of IL-20 is reduced. The method is useful for producing such
 CC therapeutic antibody. The antibody or antibody fragment, produced using
 CC the above method, binds to IL-20, and inhibits or reduces the pro-
 CC inflammatory activity of IL-20. IL-20-induced proliferation or
 CC differentiation of hematopoietic cells and hematopoietic cell progenitors
 CC may be reduced or inhibited using the antibody. Note: The specification
 CC refers to Seq ID 52 as being a primer from the 5' UTR of full length
 CC mouse IL-20RA used to generate the full length sequence. The sequence
 CC published is actually a duplicate of AEA50101 which is murine IL-20RA.
 XX Sequence 553 AA;
 SQ

Query Match 100.0%; Score 2947; DB 9; Length 553;
 Best Local Similarity 100.0%; Pred. No. 5.6e-240;
 Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGRPALRPLPPLPPLLLLLLAAAPWGRAVPCVSGGLPRPANITFLSINKNVLQWTPPE 60
 DB 1 MRAPGRPALRPLPPLPPLLLLLLAAAPWGRAVPCVSGGLPRPANITFLSINKNVLQWTPPE 60
 QY 61 GLQGVKVTYTVQYFIYQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVAIWTGTC 120
 DB 61 GLQGVKVTYTVQYFIYQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVAIWTGTC 120
 QY 121 SKWASGRFPYFLETOIGPPEVALTTDEKSIISVLTAPEKWKKNPEDLPVSMQIYSNLK 180
 DB 121 SKWASGRFPYFLETOIGPPEVALTTDEKSIISVLTAPEKWKKNPEDLPVSMQIYSNLK 180
 QY 181 YNVSVLNKSRTWSQCVTNHTLVLTLWLEPNTLYCVHVESFVPGPPRAQPSKQCARTL 240
 DB 181 YNVSVLNKSRTWSQCVTNHTLVLTLWLEPNTLYCVHVESFVPGPPRAQPSKQCARTL 240
 QY 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILYGNEDKRF 300
 DB 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILYGNEDKRF 300
 QY 301 FVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQBESEVKHL 360
 DB 301 FVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQBESEVKHL 360
 QY 361 GVASHLMEIFCDSEENTEGTSFTQBSLSRTIPDPKTVIEYDVVTTDTCAGPEQELS 420
 DB 361 GVASHLMEIFCDSEENTEGTSFTQBSLSRTIPDPKTVIEYDVVTTDTCAGPEQELS 420
 QY 421 LQEEVSTQGTLLSQALAVLGPQTLYSYTPOQLDPLAQHSDSEEGPEEPSTTLV 480
 DB 421 LQEEVSTQGTLLSQALAVLGPQTLYSYTPOQLDPLAQHSDSEEGPEEPSTTLV 480
 QY 481 DWDPTQGLRCLIPSLSSFDQDSECEPSEGDGLGEGLLSRLYEPAADPPGNETYLMQ 540
 DB 481 DWDPTQGLRCLIPSLSSFDQDSECEPSEGDGLGEGLLSRLYEPAADPPGNETYLMQ 540
 QY 541 FMEEWGLYVQMEN 553
 DB 541 FMEEWGLYVQMEN 553

RESULT 15

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 5, 2006, 11:41:13 ; Search time 24.1169 Seconds
(without alignments)
1066.146 Million cell updates/sec

Title: US-09-745-792A-14
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/prodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/prodata/1/iaa/H COMB.pep.*
4: /cgn2_6/prodata/1/iaa/PCUS COMB.pep.*
5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1644	100.0	311	2	US-09-746-359A-14
2	1644	100.0	311	2	US-09-991-181-183
3	1644	100.0	311	2	US-09-999-833A-352
4	1644	100.0	311	2	US-09-990-444-183
5	1644	100.0	311	2	US-09-997-333-183
6	1644	100.0	311	2	US-09-992-598-183
7	1644	100.0	311	2	US-10-020-445A-352
8	1620	98.5	311	2	US-09-265-540B-2
9	1477	89.8	301	2	US-09-746-359A-19
10	1234.5	75.1	336	2	US-09-746-359A-57
11	1218	74.1	229	2	US-10-233-873A-2
12	1209	73.5	352	2	US-09-746-359A-21
13	1080	65.7	203	2	US-09-746-359A-15
14	1075.5	65.4	307	2	US-09-746-359A-58
15	1069	65.0	201	2	US-09-746-359A-59
16	1061	64.5	203	2	US-09-746-359A-68
17	1050	63.9	201	2	US-09-746-359A-61
18	1050	63.6	323	2	US-09-746-359A-60
19	1046	63.6	196	2	US-09-746-359A-67
20	1027	62.5	196	2	US-09-746-359A-69
21	718	43.7	135	2	US-09-746-359A-70
22	699	42.5	135	2	US-09-746-359A-71
23	529	32.2	100	2	US-09-513-999C-7690
24	204	12.4	273	2	US-09-949-016-11056
25	204	12.4	325	1	US-08-683-743-4
26	204	12.4	325	1	US-09-870-574-3
27	204	12.4	325	2	US-09-265-540B-6

28	189.5	11.5	337	2	US-08-871-572B-1	Sequence 1, Appli
29	189.5	11.5	516	2	US-09-949-002-547	Sequence 547, App
30	188.5	11.5	337	2	US-08-871-572B-4	Sequence 4, Appli
31	188.5	11.5	337	2	US-09-265-540B-5	Sequence 5, Appli
32	188.5	11.5	337	2	US-09-949-002-383	Sequence 383, App
33	186.5	11.3	337	4	PCT-US94-14277-8	Sequence 8, Appli
34	184	11.2	258	2	US-08-871-572B-5	Sequence 5, Appli
35	174.5	10.6	557	2	US-07-971-834-4	Sequence 4, Appli
36	173.5	10.6	557	1	US-08-328-256-10	Sequence 10, Appl
37	173.5	10.6	557	1	US-08-471-454-2	Sequence 2, Appli
38	173.5	10.6	557	1	US-08-466-974-2	Sequence 2, Appli
39	173.5	10.6	557	1	US-08-471-453-2	Sequence 2, Appli
40	173.5	10.6	557	1	US-08-307-588-4	Sequence 4, Appli
41	173.5	10.6	557	2	US-09-240-675-4	Sequence 4, Appli
42	173.5	10.6	557	2	US-09-949-016-5972	Sequence 5972, Ap
43	173.5	10.6	575	2	US-09-949-016-8640	Sequence 8640, Ap
44	168	10.2	233	2	US-08-871-572B-8	Sequence 8, Appli
45	164.5	10.0	210	2	US-10-090-365-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-746-359A-14
; Sequence 14, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekhar, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-14

Query Match	100.0%	Score 1644;	DB 2;	Length 311;
Best Local Similarity	100.0%;	Pred. No. 1.8e-165;		
Matches 311;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MQFTFWLSEIWTSLFPMWFFYALIPCLLTDEVAIPAPQNLVSLSTNMKHLWMSPVIAP	60	
Db	1	MQFTFWLSEIWTSLFPMWFFYALIPCLLTDEVAIPAPQNLVSLSTNMKHLWMSPVIAP	60	
QY	61	GETVYVSVEYQGEYESLYTSHIWPSSWCSLSTEGPCDVTDDITATVPYNLRVATLGSQ	120	
Db	61	GETVYVSVEYQGEYESLYTSHIWPSSWCSLSTEGPCDVTDDITATVPYNLRVATLGSQ	120	
QY	121	TSAWSILKHPFNRRNSTILTRPGMEITKOGFHLVIELEDLGPQEFVLVAYWRPFGAEHV	180	
Db	121	TSAWSILKHPFNRRNSTILTRPGMEITKOGFHLVIELEDLGPQEFVLVAYWRPFGAEHV	180	
QY	181	KMVRSGIIPVHLETPEPGAAYCVKAOTFYKATGRYSASFQTECEVOGEAIPLVLFALFAP	240	

Db 181 KMVRSGGIPVHLETFMEPGAAYCVKAQTFVKAIGRYSAFSQTECVQGEAIPVLVLFAPF 240
Qy 241 VGFMLLTVVVPFLVFKWGRLLQYSCCPVVVLPTLKITNSPQKLISCRREVDACATAYM 300
Db 241 VGFMLLTVVVPFLVFKWGRLLQYSCCPVVVLPTLKITNSPQKLISCRREVDACATAYM 300
Qy 301 SPEELLRAWIS 311
Db 301 SPEELLRAWIS 311

RESULT 2
US-09-991-181-183
; Sequence 183, Application US/09991181
; Patent No. 6913919
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC53
; CURRENT APPLICATION NUMBER: US/09/991,181
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
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; PRIOR FILING DATE: 1998-06-17
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; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089908
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089948

1 MOTFTWVLEIWTSLFMWFFYALIPCLLTDEVAIPQNLVSLTNMKHLLMWSPIAP 60
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
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PRIOR APPLICATION NUMBER: 60/090862
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PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091798
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1644; DB 2; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.8e-165;
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MOTFTWVLEIWTSLFMWFFYALIPCLLTDEVAIPQNLVSLTNMKHLLMWSPIAP 60

Db 1 MQTFTWVLEIWTSLFMWFFYALIPCLLTDEVAIPQNLVSLTNMKHLLMWSPIAP 60
Qy 61 GETVYYSVEYQGEYESLYTSHIWPSSWCSLTEGPECDVTDITATVPYNLRVRATLGSQ 120
Db 61 GETVYYSVEYQGEYESLYTSHIWPSSWCSLTEGPECDVTDITATVPYNLRVRATLGSQ 120
Qy 121 TSAMSLKHPPFNENSTILTRPGMEITKDGPHLVIELEDLGPOPEFLVAYWRREPGEAEHV 180
Db 121 TSAMSLKHPPFNENSTILTRPGMEITKDGPHLVIELEDLGPOPEFLVAYWRREPGEAEHV 180
Qy 181 KMRVSGGIPVHLETMEPGAAYCVKAOTFVKAIGRYSAFSQTECEVQGEAIPVLALFAF 240
Db 181 KMRVSGGIPVHLETMEPGAAYCVKAOTFVKAIGRYSAFSQTECEVQGEAIPVLALFAF 240
Qy 241 VGFMLILVVVPLFVWKGRLLOYSCCPVVVLPDTLKITNSPQKLI SCRREVDACATAVM 300
Db 241 VGFMLILVVVPLFVWKGRLLOYSCCPVVVLPDTLKITNSPQKLI SCRREVDACATAVM 300
Qy 301 SPEELLRAWIS 311
Db 301 SPEELLRAWIS 311

RESULT 3

US-09-999-833A-352
; Sequence 352, Application US/09999833A
; Patent No. 6916648
; GENERAL INFORMATION: ---
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Faoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC65
; CURRENT APPLICATION NUMBER: US/09/999,833A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10


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; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      100.0%; Score 1644; DB 2; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.8e-165;
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQFTWVLEIWTSLFWMFYALIPCLLTDEVAIPAPQNLVLSTNMKHLWMSPIAP 60
   |||||
Db 1 MQFTWVLEIWTSLFWMFYALIPCLLTDEVAIPAPQNLVLSTNMKHLWMSPIAP 60
   |||||

QY 61 GETVYYSVEYQGBYESLYTSHIWPSSWCSLTGPECDVDDITATVPYNLVRATLGSQ 120
   |||||
Db 61 GETVYYSVEYQGBYESLYTSHIWPSSWCSLTGPECDVDDITATVPYNLVRATLGSQ 120
   |||||

QY 121 TSWSILKHPFNRSNTILTRPGMEITKDGPHLVIELEDLGPQFEFLVAYWRPGEAEHV 180
   |||||
Db 121 TSWSILKHPFNRSNTILTRPGMEITKDGPHLVIELEDLGPQFEFLVAYWRPGEAEHV 180
   |||||

QY 181 KMYRSGIPVHLEMTPEGAAYCVKAQTFVKAIGRYSAFSQTECVQGEAIPLVLAFAF 240
   |||||
Db 181 KMYRSGIPVHLEMTPEGAAYCVKAQTFVKAIGRYSAFSQTECVQGEAIPLVLAFAF 240
   |||||

QY 241 VGFMLILVVVPLFWKMGRLLOQSCCPVVLPDTLKITNSPQKLISCRREEVDACATAVM 300
   |||||
Db 241 VGFMLILVVVPLFWKMGRLLOQSCCPVVLPDTLKITNSPQKLISCRREEVDACATAVM 300
   |||||

QY 301 SPEELLRAWIS 311
   |||||
Db 301 SPEELLRAWIS 311
   |||||

RESULT 4
US-09-990-444-183
; Sequence 183, Application US/09990444
; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCES: P2730P1C19
; CURRENT APPLICATION NUMBER: US/09/990,444
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16

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; PRIOR FILING DATE: 1998-06-16
 ; PRIOR APPLICATION NUMBER: 60/089512
 ; PRIOR FILING DATE: 1998-06-16
 ; PRIOR APPLICATION NUMBER: 60/089514
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 ; PRIOR APPLICATION NUMBER: 60/089532
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 ; PRIOR APPLICATION NUMBER: 60/089907
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; PRIOR APPLICATION NUMBER: 60/090863
 ; PRIOR FILING DATE: 1998-06-26
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 ; PRIOR FILING DATE: 1998-07-01
 ; PRIOR APPLICATION NUMBER: 60/091478
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091544
 ; PRIOR FILING DATE: 1998-07-01
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 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091626
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 ; PRIOR APPLICATION NUMBER: 60/091633
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091978
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

 Query Match 100.0%; Score 1644; DB 2; Length 311;
 Best Local Similarity 100.0%; Pred. No. 1.8e-165; Indels 0; Gaps 0;
 Matches 311; Conservative 0; Mismatches 0;

 QY 1 MQTFTWVLEIEIWTSLFMWFFYALIPCLLTDEVAIIPAPQNLVSLSTNMKHLMMSPVIAP 60
 DB 1 MQTFTWVLEIEIWTSLFMWFFYALIPCLLTDEVAIIPAPQNLVSLSTNMKHLMMSPVIAP 60

 QY 61 GETVYVSVEYQGEYSLSYTSHTWIWIPSSWCSLSTEGPECDVTDDITATVPYNLRVATLGSQ 120
 DB 61 GETVYVSVEYQGEYSLSYTSHTWIWIPSSWCSLSTEGPECDVTDDITATVPYNLRVATLGSQ 120

 QY 121 TSAMSTLKHPPNENSTILTRPGMEITKOGFHLVIELEDLGPQEFIVAYWRREPGEAEHV 180
 DB 121 TSAMSTLKHPPNENSTILTRPGMEITKOGFHLVIELEDLGPQEFIVAYWRREPGEAEHV 180

 QY 181 KMRVSGGIPVHLETMPEPGAAYCVKAQTFVKAIGRYSASFQTECEVQGEAIPIVLALFAF 240
 DB 181 KMRVSGGIPVHLETMPEPGAAYCVKAQTFVKAIGRYSASFQTECEVQGEAIPIVLALFAF 240

 QY 241 VGFMLILVVVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLSICRREEVDACATVM 300
 DB 241 VGFMLILVVVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLSICRREEVDACATVM 300

 QY 301 SPEELLRAWIS 311
 DB 301 SPEELLRAWIS 311

 RESULT 5
 US-09-997-333-183
 ; Sequence 183, Application US/09997333
 ; Patent No. 6953836
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnovers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC27
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Query Match 100.0%; Score 1644; DB 2; Length 311;

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Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 VGFMLILVVVPLFVWKMGRLQYSCCPVVVLPDTLKITNSPKQLISCRREEVDACATVM 300
DB 241 VGFMLILVVVPLFVWKMGRLQYSCCPVVVLPDTLKITNSPKQLISCRREEVDACATVM 300
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; APPLICANT: Zhang, Zemin
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Db 301 SPEELRAWIS 311

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US-10-020-445A-352

Sequence 352, Application US/10020445A

Patent No. 6962797

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2630P1C74

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; PRIOR APPLICATION NUMBER: 60/083558
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      100.0%; Score 1644; DB 2; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.8e-165;
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1      MQTFTVLEIWTSLFWMFYALIPCLLTDEVAIPAPQNLVSLTNMKHLLMWSVPIAP 60
Db      1      MQTFTVLEIWTSLFWMFYALIPCLLTDEVAIPAPQNLVSLTNMKHLLMWSVPIAP 60

Qy      61      GETVYYSVEYQGYESLYTSHIWPSSWCSLTGPECDVTDITATVPYNLRVRATLGSQ 120
Db      61      GETVYYSVEYQGYESLYTSHIWPSSWCSLTGPECDVTDITATVPYNLRVRATLGSQ 120

Qy      121     TSAWSILKHPFNNSILTRPGMEITKDGPHLVIELEDLGQPEFLVAYWRREPGEAEHV 180

```

RESULT 8

```

US-09-265-540E-2
; Sequence 2, Application US/09265540E
; Patent No. 6586228
; GENERAL INFORMATION:
; APPLICANT: Parham, Christi L.
; APPLICANT: Moore, Kevin W.
; APPLICANT: Murgolo, Nicholas J.
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: HUMAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX0804K
; CURRENT APPLICATION NUMBER: US/09/265,540E
; CURRENT FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 60/077,329
; PRIOR FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (146)..(146)
; OTHER INFORMATION: The 'Xaa' at location 146 stands for Thr, Ala, Pro, or Ser.
; NAME/KEY: misc feature
; LOCATION: (148)..(148)
; OTHER INFORMATION: The 'Xaa' at location 148 stands for Asn, Asp, His, or Tyr.
; NAME/KEY: misc feature
; LOCATION: (171)..(171)
; OTHER INFORMATION: The 'Xaa' at location 171 stands for Arg, or Thr.
; NAME/KEY: misc feature
; LOCATION: (214)..(214)
; OTHER INFORMATION: The 'Xaa' at location 214 stands for Arg, or Lys.
; NAME/KEY: misc feature
; LOCATION: (567)..(567)
; OTHER INFORMATION: unknown nucleotide
; NAME/KEY: misc feature
; LOCATION: (573)..(573)
; OTHER INFORMATION: unknown nucleotide
; NAME/KEY: misc feature
; LOCATION: (1336)..(1336)
; OTHER INFORMATION: unknown nucleotide
; NAME/KEY: misc feature
; LOCATION: (1369)..(1369)
; OTHER INFORMATION: unknown nucleotide
US-09-265-540E-2

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Query Match      98.5%; Score 1620; DB 2; Length 311;
Best Local Similarity 98.7%; Pred. No. 6.3e-163;
Matches 307; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1      MQTFTVLEIWTSLFWMFYALIPCLLTDEVAIPAPQNLVSLTNMKHLLMWSVPIAP 60

```

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Db      1  MOTFTMWLEIWTSLFMWFFYALIPCLLTDEVAIIPAPQNLSVLSTNMKHLNWSVPIAP 60
QY      61  GETVYYSVEYQGEYESLYTSHIWPSSWCSLTGPECDVTDITATVPYNLRVRATLGSQ 120
      |||||||
Db      61  GETVYYSVEYQGEYESLYTSHIWPSSWCSLTGPECDVTDITATVPYNLRVRATLGSQ 120
      |||||||
QY      121  TSAWSILKHPFNRRNSTILTRPGMEITKDGPHLVLELDLGPQFEFLVAYWRREPGEAEHV 180
      |||||||
Db      121  TSAWSILKHPFNRRNSTILTRPGMEIKXGPHLVLELDLGPQFEFLVAYWRREPGEAEHV 180
      |||||||
QY      181  KMRVSGGIPVHLETMEPGAAYCVKAOTFVKAIGRYSAFSQTECVQGEAIPLVLALFAP 240
      |||||||
Db      181  KMRVSGGIPVHLETMEPGAAYCVKAOTFVKAIGRYSAFSQTECVQGEAIPLVLALFAP 240
      |||||||
QY      241  VGFMILLVVVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLSRREEVDACATVM 300
      |||||||
Db      241  VGFMILLVVVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLSRREEVDACATVM 300
      |||||||
QY      301  SPEELRAWIS 311
      |||||||
Db      301  SPEELRAWIS 311
      |||||||

RESULT 9
US-09-746-359A-19
; Sequence 19, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-19

Query Match      89.8%; Score 1477; DB 2; Length 301;
Best Local Similarity 98.9%; Pred. No. 8.2e-148;
Matches 279; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  MOTFTMWLEIWTSLFMWFFYALIPCLLTDEVAIIPAPQNLSVLSTNMKHLNWSVPIAP 60
Db      1  MOTFTMWLEIWTSLFMWFFYALIPCLLTDEVAIIPAPQNLSVLSTNMKHLNWSVPIAP 60
      |||||||
QY      61  GETVYYSVEYQGEYESLYTSHIWPSSWCSLTGPECDVTDITATVPYNLRVRATLGSQ 120
Db      61  GETVYYSVEYQGEYESLYTSHIWPSSWCSLTGPECDVTDITATVPYNLRVRATLGSQ 120
      |||||||
QY      121  TSAWSILKHPFNRRNSTILTRPGMEITKDGPHLVLELDLGPQFEFLVAYWRREPGEAEHV 180
Db      121  TSAWSILKHPFNRRNSTILTRPGMEIPKHGPHLVLELDLGPQFEFLVAYWRREPGEAEHV 180
      |||||||
QY      181  KMRVSGGIPVHLETMEPGAAYCVKAOTFVKAIGRYSAFSQTECVQGEAIPLVLALFAP 240
      |||||||
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```
Db      181  KMRVSGGIPVHLETMEPGAAYCVKAOTFVKAIGRYSAFSQTECVQGEAIPLVLALFAP 240
QY      241  VGFMILLVVVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQ 282
      |||||||
Db      241  VGFMILLVVVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQ 282
      |||||||

RESULT 10
US-09-746-359A-57
; Sequence 57, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 57
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-57

Query Match      75.1%; Score 1234.5; DB 2; Length 336;
Best Local Similarity 85.9%; Pred. No. 4.6e-122;
Matches 238; Conservative 7; Mismatches 17; Indels 15; Gaps 2;

QY      1  MOTFTMWLEIWTSLFMWFFYALIPCLLTDEVAIIPAPQNLSVLSTNMKHLNWSVPIAP 60
Db      1  MOTFTMWLEIWTSLFMWFFYALIPCLLTDEVAIIPAPQNLSVLSTNMKHLNWSVPIAP 60
      |||||||
QY      61  GETVYYSVEYQGEYESLYTSHIWPSSWCSLTGPECDVTDITATVPYNLRVRATLGSQ 120
Db      61  GETVYYSVEYQGEYESLYTSHIWPSSWCSLTGPECDVTDITATVPYNLRVRATLGSQ 120
      |||||||
QY      121  TSAWSILKHPFNRRNSTILTRPGMEITKDGPHLVLELDLGPQFEFLVAYWRREPGEAEHV 180
Db      121  TSAWSILKHPFNRRNSTILTRPGMEITKDGPHLVLELDLGPQFEFLVAYWRREPGEAEHV 180
      |||||||
QY      181  KMRVSGGIPVHLETMEPGAAYCVKAOTFVKAIGRYSAFSQTECVQGEAIPLVLALFAP 240
Db      181  KMRVSGGIPVHLETMEPGAAYCVKAOTFVKAIGRYSAFSQTECVQGEATVAAPSVFIF 240
      |||||||
QY      241  -----VGFMILLVVVPLFV-----WKMGRLQ 262
      |||||
Db      241  PPSDEQLKSGTASVVCLLNNFYPREAKVQMKVDNALQ 277
      |||||

RESULT 11
US-10-233-873A-2
; Sequence 2, Application US/10233873A
; Patent No. 6902930
; GENERAL INFORMATION:
; APPLICANT: Peng Liang
; TITLE OF INVENTION: THE HUMAN MOB-5 (IL-24) RECEPTORS AND USES THEREOF
; FILE REFERENCE: 22000.0091U4
; CURRENT APPLICATION NUMBER: US/10/233,873A
```



```
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 58
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-58
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Query Match 65.4%; Score 1075.5; DB 2; Length 307;
Best Local Similarity 84.3%; Pred. No. 2.7e-105;
Matches 209; Conservative 7; Mismatches 17; Indels 15; Gaps 2;

QY 30 DEVAIIAPQNLSVLSTNNKHLIWMSPVIAPGETVYYSVEYQGEYESLYTSHIWPSSWC 89
Db 1 DEVAIIAPQNLSVLSTNNKHLIWMSPVIAPGETVYYSVEYQGEYESLYTSHIWPSSWC 60

QY 90 SLTEGPECDVTDITATVPYNLRVRATLGSQTSAMSIKXHPFNRNSTILTRPGMEITKDG 149
Db 61 SLTEGPECDVTDITATVPYNLRVRATLGSQTSAMSIKXHPFNRNSTILTRPGMEITKDG 120

QY 150 FHLVIELEDLGPQFEFLVAYWRREPGEAEHVKMVRSGGIPVHLETMEPGAAAYCVKAQTFV 209
Db 121 FHLVIELEDLGPQFEFLVAYWRREPGEAEHVKMVRSGGIPVHLETMEPGAAAYCVKAQTFV 180

QY 210 KAIGRYSAFSQTECVQGEATPLVLALPAF-----VGFMLILVVVPLFV----- 254
Db 181 KAIGRYSAFSQTECVQGEATVAAPSVIFPPSDQLKSGTASVVCLLNNFYPREAKVQ 240

QY 255 WKMGRLQ 262
Db 241 WKVDNALQ 248
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RESULT 15
US-09-746-359A-59
; Sequence 59, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
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; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-59

Query Match 65.0%; Score 1069; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 7e-105;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 DEVAIIAPQNLSVLSTNNKHLIWMSPVIAPGETVYYSVEYQGEYESLYTSHIWPSSWC 89
Db 1 DEVAIIAPQNLSVLSTNNKHLIWMSPVIAPGETVYYSVEYQGEYESLYTSHIWPSSWC 60

QY 90 SLTEGPECDVTDITATVPYNLRVRATLGSQTSAMSIKXHPFNRNSTILTRPGMEITKDG 149
Db 61 SLTEGPECDVTDITATVPYNLRVRATLGSQTSAMSIKXHPFNRNSTILTRPGMEITKDG 120

QY 150 FHLVIELEDLGPQFEFLVAYWRREPGEAEHVKMVRSGGIPVHLETMEPGAAAYCVKAQTFV 209
Db 121 FHLVIELEDLGPQFEFLVAYWRREPGEAEHVKMVRSGGIPVHLETMEPGAAAYCVKAQTFV 180

QY 210 KAIGRYSAFSQTECVQGEA 230
Db 181 KAIGRYSAFSQTECVQGEA 201

Search completed: April 5, 2006, 11:42:59
Job time : 25.1169 secs
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OM protein - protein search, using sw model

Run on: April 5, 2006, 11:41:13 ; Search time 42.8831 Seconds
(without alignments)
1066.146 Million cell updates/sec

Title: US-09-745-792A-11

Perfect score: 2947

Sequence: 1 MRAPGRPALRPPLPPLLLL.....NETYLMQFMEEWGLYQVMEN 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/ptodata/1/iaa/6-COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/H-COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/PCTUS-COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/RE-COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2947	100.0	553	1	US-08-943-087-2
2	2947	100.0	553	1	US-08-943-087-14
3	2947	100.0	553	1	US-08-943-087-16
4	2947	100.0	553	1	US-08-943-087-18
5	2947	100.0	553	1	US-08-943-087-20
6	2947	100.0	553	1	US-08-943-087-22
7	2947	100.0	553	1	US-08-943-087-24
8	2947	100.0	553	1	US-08-943-087-26
9	2947	100.0	553	1	US-08-943-087-28
10	2947	100.0	553	1	US-08-943-087-30
11	2947	100.0	553	1	US-08-943-087-32
12	2947	100.0	553	1	US-08-943-087-34
13	2947	100.0	553	1	US-08-943-087-36
14	2947	100.0	553	1	US-08-943-087-38
15	2947	100.0	553	1	US-08-943-087-40
16	2947	100.0	553	1	US-08-943-087-42
17	2947	100.0	553	1	US-08-943-087-44
18	2947	100.0	553	1	US-08-943-087-46
19	2947	100.0	553	1	US-08-943-087-48
20	2947	100.0	553	2	US-09-746-359A-11
21	2947	100.0	553	2	US-09-861-779-2
22	2947	100.0	553	2	US-09-949-016-6873
23	2947	100.0	553	2	US-10-233-873A-7
24	2941	99.8	567	2	US-09-949-016-11502
25	2203	74.8	442	2	US-10-012-231A-104
26	2203	74.8	442	2	US-10-015-389A-104
27	2203	74.8	442	2	US-10-006-768A-104

28 2203 74.8 442 2 US-10-015-671A-104 Sequence 104, App

29 2203 74.8 442 2 US-10-015-393A-104 Sequence 104, App

30 2203 74.8 442 2 US-10-011-833A-104 Sequence 104, App

31 2203 74.8 442 2 US-10-006-041A-104 Sequence 104, App

32 2203 74.8 442 2 US-10-012-064A-104 Sequence 104, App

33 1769.5 60.0 546 2 US-09-746-359A-37 Sequence 37, Appl

34 1715 58.2 514 2 US-09-746-359A-39 Sequence 39, Appl

35 1344 45.6 248 2 US-10-233-873A-3 Sequence 3, Appl

36 1294.5 43.9 571 2 US-09-746-359A-53 Sequence 53, Appl

37 1200 40.7 221 1 US-08-943-087-50 Sequence 50, Appl

38 1200 40.7 221 1 US-09-746-359A-12 Sequence 12, Appl

39 1196 40.6 221 1 US-08-943-087-54 Sequence 54, Appl

40 1192 40.4 221 1 US-08-943-087-52 Sequence 52, Appl

41 1184 40.2 221 1 US-08-943-087-56 Sequence 56, Appl

42 1183 40.1 547 2 US-09-746-359A-54 Sequence 54, Appl

43 1182 40.1 221 1 US-08-943-087-58 Sequence 58, Appl

44 1180 40.0 217 2 US-09-746-359A-55 Sequence 55, Appl

45 1171 39.7 594 2 US-09-746-359A-23 Sequence 23, Appl

ALIGNMENTS

RESULT 1

US-08-943-087-2
; Sequence 2, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-943-087-2

Query Match 100.0%; Score 2947; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.6e-267;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGRPALRPLPLPPLLLLLLAAPMGRAVPVCVSGGLPKPANITFLSINMKVLTWTPPE 60
DB 1 MRAPGRPALRPLPLPPLLLLLLAAPMGRAVPVCVSGGLPKPANITFLSINMKVLTWTPPE 60

QY 61 GLQGVKVTYTVQYFIYGQKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAIMGTKC 120
DB 61 GLQGVKVTYTVQYFIYGQKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAIMGTKC 120

QY 121 SKWASGRFYPFLETOIGPPEVALTTDEKSI SVLTAPKWKENPEDLPVSMQOIYSNLK 180
DB 121 SKWASGRFYPFLETOIGPPEVALTTDEKSI SVLTAPKWKENPEDLPVSMQOIYSNLK 180

QY 181 YNVSVLNRTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQCARLT 240
DB 181 YNVSVLNRTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQCARLT 240

QY 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILYGNEDFKRF 300
DB 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILYGNEDFKRF 300

QY 301 FVPAEKIVINFITLNISSDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEESEVKHL 360
DB 301 FVPAEKIVINFITLNISSDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEESEVKHL 360

QY 361 GYASHLMEIFCDSEENTEGTSFTQBSLSRTIPPDKTVIYEYDVVTTDTCAGPEQEELS 420
DB 361 GYASHLMEIFCDSEENTEGTSFTQBSLSRTIPPDKTVIYEYDVVTTDTCAGPEQEELS 420

QY 421 LQEEVSTQGTLLSQAAALVGLPQTLYSYTQQLDPLAQEHTDSEGEPEEPSTTLV 480
DB 421 LQEEVSTQGTLLSQAAALVGLPQTLYSYTQQLDPLAQEHTDSEGEPEEPSTTLV 480

QY 481 DWDPTQGRLCIPSLSSFDQDSECEPSEGDGLGEEGLLSRLYEAPADPPGGENETVLMQ 540
DB 481 DWDPTQGRLCIPSLSSFDQDSECEPSEGDGLGEEGLLSRLYEAPADPPGGENETVLMQ 540

QY 541 FMEEWGLYQOMEN 553
DB 541 FMEEWGLYQOMEN 553

RESULT 2

US-08-943-087-14
; Sequence 14, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-08-943-087-14

Query Match 100.0%; Score 2947; DB 1; Length 553;

Best Local Similarity 100.0%; Pred. No. 1.6e-267;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGRPALRPLPLPPLLLLLLAAPMGRAVPVCVSGGLPKPANITFLSINMKVLTWTPPE 60
DB 1 MRAPGRPALRPLPLPPLLLLLLAAPMGRAVPVCVSGGLPKPANITFLSINMKVLTWTPPE 60

QY 61 GLQGVKVTYTVQYFIYGQKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAIMGTKC 120
DB 61 GLQGVKVTYTVQYFIYGQKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAIMGTKC 120

QY 121 SKWASGRFYPFLETOIGPPEVALTTDEKSI SVLTAPKWKENPEDLPVSMQOIYSNLK 180
DB 121 SKWASGRFYPFLETOIGPPEVALTTDEKSI SVLTAPKWKENPEDLPVSMQOIYSNLK 180

QY 181 YNVSVLNRTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQCARLT 240
DB 181 YNVSVLNRTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQCARLT 240

QY 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILYGNEDFKRF 300
DB 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILYGNEDFKRF 300

QY 301 FVPAEKIVINFITLNISSDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEESEVKHL 360
DB 301 FVPAEKIVINFITLNISSDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEESEVKHL 360

QY 361 GYASHLMEIFCDSEENTEGTSFTQBSLSRTIPPDKTVIYEYDVVTTDTCAGPEQEELS 420
DB 361 GYASHLMEIFCDSEENTEGTSFTQBSLSRTIPPDKTVIYEYDVVTTDTCAGPEQEELS 420

QY 421 LQEEVSTQGTLLSQAAALVGLPQTLYSYTQQLDPLAQEHTDSEGEPEEPSTTLV 480
DB 421 LQEEVSTQGTLLSQAAALVGLPQTLYSYTQQLDPLAQEHTDSEGEPEEPSTTLV 480

QY 481 DWDPTQGRLCIPSLSSFDQDSECEPSEGDGLGEEGLLSRLYEAPADPPGGENETVLMQ 540
DB 481 DWDPTQGRLCIPSLSSFDQDSECEPSEGDGLGEEGLLSRLYEAPADPPGGENETVLMQ 540

QY 541 FMEEWGLYQOMEN 553
DB 541 FMEEWGLYQOMEN 553

RESULT 3

US-08-943-087-16
; Sequence 16, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si

QY 61 GLQGVKVTYVQYFYIYGQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVKAIWGTC 120
DB 61 GLQGVKVTYVQYFYIYGQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVKAIWGTC 120
QY 121 SKWASGRYPFLETQIGPPEVALTTDEKSI SVLTAPEKWKRNPDLPVSMQOIYSNLK 180
DB 121 SKWASGRYPFLETQIGPPEVALTTDEKSI SVLTAPEKWKRNPDLPVSMQOIYSNLK 180
QY 181 YNVSVLNKTNSRTWOCVTNHTLVLTLWLPNTLYCVHVESFVPGPRRAQPKSEKQCARTL 240
DB 181 YNVSVLNKTNSRTWOCVTNHTLVLTLWLPNTLYCVHVESFVPGPRRAQPKSEKQCARTL 240
QY 241 KDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILYIGNEFDKRF 300
DB 241 KDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILYIGNEFDKRF 300
QY 301 FVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQSGNLRLPPOEEBEVKHL 360
DB 301 FVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQSGNLRLPPOEEBEVKHL 360
QY 361 GYASHLMEIFCDSEENTEGTSFTQESLSRTIPPDKTVIEYDVRTTDCAGPEEQELS 420
DB 361 GYASHLMEIFCDSEENTEGTSFTQESLSRTIPPDKTVIEYDVRTTDCAGPEEQELS 420
QY 421 LOEEVSTQGTLLSQAALAVLGPQTLYQSYTTPQLQDLPLAQEHDTSEEGPEEPSTTLV 480
DB 421 LOEEVSTQGTLLSQAALAVLGPQTLYQSYTTPQLQDLPLAQEHDTSEEGPEEPSTTLV 480
QY 481 DNDPQTRGLCIPSLSFDDQSGCEPSEGDGLGEEGLLSRLYEAPADPPGNETYLMQ 540
DB 481 DNDPQTRGLCIPSLSFDDQSGCEPSEGDGLGEEGLLSRLYEAPADPPGNETYLMQ 540
QY 541 FMEEWGLYVQMEN 553
DB 541 FMEEWGLYVQMEN 553

RESULT 5

US-08-943-087-20
; Sequence 20, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743

; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-943-087-20

Query Match 100.0%; Score 2947; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.6e-267;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRAPGRPALRPLPPLLLLLLAAAPWGRAVPCVSGGLPKPANITFLSINKNVLTQTPPE 60
DB 1 MRAPGRPALRPLPPLLLLLLAAAPWGRAVPCVSGGLPKPANITFLSINKNVLTQTPPE 60
QY 61 GLQGVKVTYVQYFYIYGQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVKAIWGTC 120
DB 61 GLQGVKVTYVQYFYIYGQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVKAIWGTC 120
QY 121 SKWASGRYPFLETQIGPPEVALTTDEKSI SVLTAPEKWKRNPDLPVSMQOIYSNLK 180
DB 121 SKWASGRYPFLETQIGPPEVALTTDEKSI SVLTAPEKWKRNPDLPVSMQOIYSNLK 180
QY 181 YNVSVLNKTNSRTWOCVTNHTLVLTLWLPNTLYCVHVESFVPGPRRAQPKSEKQCARTL 240
DB 181 YNVSVLNKTNSRTWOCVTNHTLVLTLWLPNTLYCVHVESFVPGPRRAQPKSEKQCARTL 240
QY 241 KDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILYIGNEFDKRF 300
DB 241 KDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILYIGNEFDKRF 300
QY 301 FVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQSGNLRLPPOEEBEVKHL 360
DB 301 FVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQSGNLRLPPOEEBEVKHL 360
QY 361 GYASHLMEIFCDSEENTEGTSFTQESLSRTIPPDKTVIEYDVRTTDCAGPEEQELS 420
DB 361 GYASHLMEIFCDSEENTEGTSFTQESLSRTIPPDKTVIEYDVRTTDCAGPEEQELS 420
QY 421 LOEEVSTQGTLLSQAALAVLGPQTLYQSYTTPQLQDLPLAQEHDTSEEGPEEPSTTLV 480
DB 421 LOEEVSTQGTLLSQAALAVLGPQTLYQSYTTPQLQDLPLAQEHDTSEEGPEEPSTTLV 480
QY 481 DNDPQTRGLCIPSLSFDDQSGCEPSEGDGLGEEGLLSRLYEAPADPPGNETYLMQ 540
DB 481 DNDPQTRGLCIPSLSFDDQSGCEPSEGDGLGEEGLLSRLYEAPADPPGNETYLMQ 540
QY 541 FMEEWGLYVQMEN 553
DB 541 FMEEWGLYVQMEN 553

RESULT 6

US-08-943-087-22
; Sequence 22, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: ZymoGenetics, Inc.
;; STREET: 1201 Eastlake Avenue East
;; CITY: Seattle
;; STATE: WA
;; COUNTRY: USA
;; ZIP: 98102
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/943,087
;; FILING DATE:
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/803,305
;; FILING DATE: 20-FEB-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lunn, Paul G
;; REGISTRATION NUMBER: 32,743
;; REFERENCE/DOCKET NUMBER: 96-24C1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 206-442-6627
;; TELEFAX: 206-442-6678
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 22:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 553 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FRAGMENT TYPE: internal
;; US-08-943-087-22

Query Match 100.0%; Score 2947; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.6e-267;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGRPALRPLPPLLLLLLAAAPWGRAVPCVSGGLPKPANITFLSINKNVLOWTPPE 60
Db 1 MRAPGRPALRPLPPLLLLLLAAAPWGRAVPCVSGGLPKPANITFLSINKNVLOWTPPE 60
QY 61 GLQGVKVTYTVQYFYIGQKKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAIWGTC 120
Db 61 GLQGVKVTYTVQYFYIGQKKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAIWGTC 120
QY 121 SKWASGRYPFLETQIGPPEVALTTDEKSI SVLTAPKWKRNRPDLPVSMQOIYSNLK 180
Db 121 SKWASGRYPFLETQIGPPEVALTTDEKSI SVLTAPKWKRNRPDLPVSMQOIYSNLK 180
QY 181 YNVSVLNTKSNRTWSQCVNTHLTVLTWLPNTLYCVHVSFVPGPPRAQPKQKARTL 240
Db 181 YNVSVLNTKSNRTWSQCVNTHLTVLTWLPNTLYCVHVSFVPGPPRAQPKQKARTL 240
QY 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIVHVGKEKHPANLILYGNFDPKRF 300
Db 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIVHVGKEKHPANLILYGNFDPKRF 300
QY 301 FVPAEKIVINFITLNTSDSKISHQMSLLGKSSDVSSNDPQPSGNLRPPQEEBEVKHL 360
Db 301 FVPAEKIVINFITLNTSDSKISHQMSLLGKSSDVSSNDPQPSGNLRPPQEEBEVKHL 360
QY 361 GYASHLMIEFCDSSENETGSTFQOESLRTIPDKTVIEYDVVTTDTCAGPEOELS 420
Db 361 GYASHLMIEFCDSSENETGSTFQOESLRTIPDKTVIEYDVVTTDTCAGPEOELS 420
QY 421 LOEEVSTQGTLLSQAALAVLGPOTQYSVTPQQLDPLAQBHTDSERGPPEEPSTTLV 480
Db 421 LOEEVSTQGTLLSQAALAVLGPOTQYSVTPQQLDPLAQBHTDSERGPPEEPSTTLV 480

QY 481 DWDPTGRLCIPSLSSFDQDSECEPSEGDGLGEEGLSRLYEPPAPDRPPGNETYLMQ 540
Db 481 DWDPTGRLCIPSLSSFDQDSECEPSEGDGLGEEGLSRLYEPPAPDRPPGNETYLMQ 540
QY 541 FMEEWGLYQVOMEN 553
Db 541 FMEEWGLYQVOMEN 553

RESULT 7
US-08-943-087-24
; Sequence 24, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-943-087-24

Query Match 100.0%; Score 2947; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.6e-267;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGRPALRPLPPLLLLLLAAAPWGRAVPCVSGGLPKPANITFLSINKNVLOWTPPE 60
Db 1 MRAPGRPALRPLPPLLLLLLAAAPWGRAVPCVSGGLPKPANITFLSINKNVLOWTPPE 60
QY 61 GLQGVKVTYTVQYFYIGQKKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAIWGTC 120
Db 61 GLQGVKVTYTVQYFYIGQKKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAIWGTC 120
QY 121 SKWASGRYPFLETQIGPPEVALTTDEKSI SVLTAPKWKRNRPDLPVSMQOIYSNLK 180

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Db 121 SKWASGRYPFLETOIGPPEVALTTDEKSI SVLTAPEKWKKNPEDLPVSMQOIYSNLK 180
QY 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQKQARTL 240
Db 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQKQARTL 240
QY 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILIYGNEDFKRF 300
Db 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILIYGNEDFKRF 300
QY 301 FVPAEKIVINFITLNTSDSKISHQMSLLGKSSDVSSLNDPQSGNLPRPQEESEVKHL 360
Db 301 FVPAEKIVINFITLNTSDSKISHQMSLLGKSSDVSSLNDPQSGNLPRPQEESEVKHL 360
QY 361 GYASHLMEIFCDSEENTEGTSFTQESLSRTIPPDKTIVIEYDVRTTIDICAGPEQELS 420
Db 361 GYASHLMEIFCDSEENTEGTSFTQESLSRTIPPDKTIVIEYDVRTTIDICAGPEQELS 420
QY 421 LQEEVSTQGTLLSQAALAVLGPQTLYSYTTPQLQDLPLAQHTDSEEGPEEPSTTLV 480
Db 421 LQEEVSTQGTLLSQAALAVLGPQTLYSYTTPQLQDLPLAQHTDSEEGPEEPSTTLV 480
QY 481 DWDPTQGRLCIPSLSSFDQDSEGCPSSEGDGLGEEGLSRLYEPAAPDRPPGNETYLMQ 540
Db 481 DWDPTQGRLCIPSLSSFDQDSEGCPSSEGDGLGEEGLSRLYEPAAPDRPPGNETYLMQ 540
QY 541 FMEEWGLYVQMEN 553
Db 541 FMEEWGLYVQMEN 553
```

RESULT 8

```
US-08-943-087-26
; Sequence 26, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-943-087-26

Query Match 100.0%; Score 2947; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.6e-267;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGRPALRPLPLPPLLLLLAAMPWGRAVPCVSGGLPKPANITFISINMKNVLTWTPPE 60
Db 1 MRAPGRPALRPLPLPPLLLLLAAMPWGRAVPCVSGGLPKPANITFISINMKNVLTWTPPE 60
QY 61 GLQGVKVTYTVQYFIYGQKKWLKSECRNINITYCDLSAETSDYEHQYAKVAIWGTK 120
Db 61 GLQGVKVTYTVQYFIYGQKKWLKSECRNINITYCDLSAETSDYEHQYAKVAIWGTK 120
QY 121 SKWASGREYFPLETOIGPPEVALTTDEKSI SVLTAPEKWKKNPEDLPVSMQOIYSNLK 180
Db 121 SKWASGREYFPLETOIGPPEVALTTDEKSI SVLTAPEKWKKNPEDLPVSMQOIYSNLK 180
QY 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQKQARTL 240
Db 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQKQARTL 240
QY 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILIYGNEDFKRF 300
Db 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILIYGNEDFKRF 300
QY 301 FVPAEKIVINFITLNTSDSKISHQMSLLGKSSDVSSLNDPQSGNLPRPQEESEVKHL 360
Db 301 FVPAEKIVINFITLNTSDSKISHQMSLLGKSSDVSSLNDPQSGNLPRPQEESEVKHL 360
QY 361 GYASHLMEIFCDSEENTEGTSFTQESLSRTIPPDKTIVIEYDVRTTIDICAGPEQELS 420
Db 361 GYASHLMEIFCDSEENTEGTSFTQESLSRTIPPDKTIVIEYDVRTTIDICAGPEQELS 420
QY 421 LQEEVSTQGTLLSQAALAVLGPQTLYSYTTPQLQDLPLAQHTDSEEGPEEPSTTLV 480
Db 421 LQEEVSTQGTLLSQAALAVLGPQTLYSYTTPQLQDLPLAQHTDSEEGPEEPSTTLV 480
QY 481 DWDPTQGRLCIPSLSSFDQDSEGCPSSEGDGLGEEGLSRLYEPAAPDRPPGNETYLMQ 540
Db 481 DWDPTQGRLCIPSLSSFDQDSEGCPSSEGDGLGEEGLSRLYEPAAPDRPPGNETYLMQ 540
QY 541 FMEEWGLYVQMEN 553
Db 541 FMEEWGLYVQMEN 553
```

RESULT 9

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US-08-943-087-28
; Sequence 28, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
```

```
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/943,087
;; FILING DATE:
;; CLASSIFICATION: 536
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: 08/803,305
;; FILING DATE: 20-FEB-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lunn, Paul G
;; REGISTRATION NUMBER: 32,743
;; REFERENCE/DOCKET NUMBER: 96-24C1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 206-442-6627
;; TELEFAX: 206-442-6678
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 28:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 553 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FRAGMENT TYPE: internal
;; US-08-943-087-28

Query Match 100.0%; Score 2947; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.6e-267;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGRPALRPLPPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLTWTPPE 60
DB 1 MRAPGRPALRPLPPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLTWTPPE 60
QY 61 GLOGKVTVTVQVFIYGQKKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAIWGTKC 120
DB 61 GLOGKVTVTVQVFIYGQKKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAIWGTKC 120
QY 121 SKWASGRFPFLETOIGPPEVALTTDEKSI SVLTAPEKWKKNPDLPVSMQOIYSNLK 180
DB 121 SKWASGRFPFLETOIGPPEVALTTDEKSI SVLTAPEKWKKNPDLPVSMQOIYSNLK 180
QY 181 YNVSVLTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQCARTL 240
DB 181 YNVSVLTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQCARTL 240
QY 241 KQOSSEFKAKIIPWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILYGNFDFKRF 300
DB 241 KQOSSEFKAKIIPWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILYGNFDFKRF 300
QY 301 FVPAEKIVNFTLNISDDSKISHQDMSLLGKSSDVSSLNDDPOPSGNLRPPQBEERVKHL 360
DB 301 FVPAEKIVNFTLNISDDSKISHQDMSLLGKSSDVSSLNDDPOPSGNLRPPQBEERVKHL 360
QY 361 GYASHLMEIFCDSEENTEGTSFTQOSLSRTIIPDKTIVIEYDVYDVTDDICAPESQELS 420
DB 361 GYASHLMEIFCDSEENTEGTSFTQOSLSRTIIPDKTIVIEYDVYDVTDDICAPESQELS 420
QY 421 LQEVSTQGTLLSQAALAVLGQTTLQYSYTPQLQDLPLAQHTDSEEGPEEPSTTLV 480
DB 421 LQEVSTQGTLLSQAALAVLGQTTLQYSYTPQLQDLPLAQHTDSEEGPEEPSTTLV 480
QY 481 DWDPTQGRICPSLSFDDQSEGCSESGDGLGEGLLSLYEEPADPPPGNETYLMQ 540
DB 481 DWDPTQGRICPSLSFDDQSEGCSESGDGLGEGLLSLYEEPADPPPGNETYLMQ 540
QY 541 FMEEWGLYVQMEN 553
DB 541 FMEEWGLYVQMEN 553
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RESULT 10
US-08-943-087-30
; Sequence 30, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-943-087-30

Query Match 100.0%; Score 2947; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.6e-267;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGRPALRPLPPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLTWTPPE 60
DB 1 MRAPGRPALRPLPPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLTWTPPE 60
QY 61 GLOGKVTVTVQVFIYGQKKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAIWGTKC 120
DB 61 GLOGKVTVTVQVFIYGQKKWLKNSCRNINRTYCDLSAETSDYEHQYAKVKAIWGTKC 120
QY 121 SKWASGRFPFLETOIGPPEVALTTDEKSI SVLTAPEKWKKNPDLPVSMQOIYSNLK 180
DB 121 SKWASGRFPFLETOIGPPEVALTTDEKSI SVLTAPEKWKKNPDLPVSMQOIYSNLK 180
QY 181 YNVSVLTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQCARTL 240
DB 181 YNVSVLTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQCARTL 240
QY 241 KQOSSEFKAKIIPWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILYGNFDFKRF 300
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Db 241 KQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILLYGNEFDKRF 300
Qy 301 FVPAEKIVINFITLNISSDSDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEESEVKHL 360
Db 301 FVPAEKIVINFITLNISSDSDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEESEVKHL 360
Qy 361 GYASHLMEIFCDSEENETGTSFTQOESLSRTTIPDKTVIEYEDVVRTTIDICAGPEQELS 420
Db 361 GYASHLMEIFCDSEENETGTSFTQOESLSRTTIPDKTVIEYEDVVRTTIDICAGPEQELS 420
Qy 421 LQEEVSTQGTLLSQAAALAVLPQTLYSYTTPQLQDLPLAQEHTDSESGPEEPSTTLV 480
Db 421 LQEEVSTQGTLLSQAAALAVLPQTLYSYTTPQLQDLPLAQEHTDSESGPEEPSTTLV 480
Qy 481 DWDPTQGRLCIPSLSFDDQSGCEPSEGDGLGEGLLSRLYEAPDRPPGENETYLMO 540
Db 481 DWDPTQGRLCIPSLSFDDQSGCEPSEGDGLGEGLLSRLYEAPDRPPGENETYLMO 540
Qy 541 FMEEWGLYVQMEN 553
Db 541 FMEEWGLYVQMEN 553

RESULT 11
US-08-943-087-32
; Sequence 32, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-943-087-32

Query Match 100.0%; Score 2947; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.6e-267;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRAPGRPALRPLPLPPLLLLLAAAPWGRAVPCVSGGLPKPANITFLSIINMKNVLQWTPPE 60
Db 1 MRAPGRPALRPLPLPPLLLLLAAAPWGRAVPCVSGGLPKPANITFLSIINMKNVLQWTPPE 60
Qy 61 GLOGVKVTVTVQYFIYGOKKWLKSECRNINITYCDLSAETSDYEHQYAKVKAINGTKC 120
Db 61 GLOGVKVTVTVQYFIYGOKKWLKSECRNINITYCDLSAETSDYEHQYAKVKAINGTKC 120
Qy 121 SKWASRGREYFLETOIGPPEVALTTDEKSI SVLTAPEKWKRNRPDLFPVSMQOIYSNLK 180
Db 121 SKWASRGREYFLETOIGPPEVALTTDEKSI SVLTAPEKWKRNRPDLFPVSMQOIYSNLK 180
Qy 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLPNTLYCVHVESFVPGPPRRAPQSEKQCARTL 240
Db 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLPNTLYCVHVESFVPGPPRRAPQSEKQCARTL 240
Qy 241 KDOSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILLYGNEFDKRF 300
Db 241 KDOSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILLYGNEFDKRF 300
Qy 301 FVPAEKIVINFITLNISSDSDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEESEVKHL 360
Db 301 FVPAEKIVINFITLNISSDSDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEESEVKHL 360
Qy 361 GYASHLMEIFCDSEENETGTSFTQOESLSRTTIPDKTVIEYEDVVRTTIDICAGPEQELS 420
Db 361 GYASHLMEIFCDSEENETGTSFTQOESLSRTTIPDKTVIEYEDVVRTTIDICAGPEQELS 420
Qy 421 LQEEVSTQGTLLSQAAALAVLPQTLYSYTTPQLQDLPLAQEHTDSESGPEEPSTTLV 480
Db 421 LQEEVSTQGTLLSQAAALAVLPQTLYSYTTPQLQDLPLAQEHTDSESGPEEPSTTLV 480
Qy 481 DWDPTQGRLCIPSLSFDDQSGCEPSEGDGLGEGLLSRLYEAPDRPPGENETYLMO 540
Db 481 DWDPTQGRLCIPSLSFDDQSGCEPSEGDGLGEGLLSRLYEAPDRPPGENETYLMO 540
Qy 541 FMEEWGLYVQMEN 553
Db 541 FMEEWGLYVQMEN 553

RESULT 12
US-08-943-087-34
; Sequence 34, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087

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; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-943-087-34

Query Match 100.0%; Score 2947; DB 1; Length 553;
Best local Similarity 100.0%; Pred. No. 1.6e-267; Indels 0; Gaps 0;
Matches 553; Conservative 0; Mismatches 0;

Qy 1 MRAPGRPALRPLPPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPE 60
Db 1 MRAPGRPALRPLPPLPPLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPE 60

Qy 61 GLOGVKVITYVOYFIYGQKKWLKSECRNINRTYCDLSAETSDYEHQYVAKVIAWGTGC 120
Db 61 GLOGVKVITYVOYFIYGQKKWLKSECRNINRTYCDLSAETSDYEHQYVAKVIAWGTGC 120

Qy 121 SKWASGRFYFLETOIGPPEVALTTDEKSI SVLVTAPEKKWRNPEDLPVSMQIYSNLK 180
Db 121 SKWASGRFYFLETOIGPPEVALTTDEKSI SVLVTAPEKKWRNPEDLPVSMQIYSNLK 180

Qy 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQCARTL 240
Db 181 YNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQCARTL 240

Qy 241 KDQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILYGNFEFKRF 300
Db 241 KDQSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIYHVGEKHPANLILYGNFEFKRF 300

Qy 301 FVPAEKIVINPITLNI SDDSKI SHQDMSLLGKSSDVSSLNDPQSGNLRPPQEEEEVKHL 360
Db 301 FVPAEKIVINPITLNI SDDSKI SHQDMSLLGKSSDVSSLNDPQSGNLRPPQEEEEVKHL 360

Qy 361 GYASHLMEIFCDSENTGTSFTQOESLSRTIPDKTVIEYEDVTRTDDICAGPEEOELS 420
Db 361 GYASHLMEIFCDSENTGTSFTQOESLSRTIPDKTVIEYEDVTRTDDICAGPEEOELS 420

Qy 421 LQEEVSTQGTLLESQAALAVLGPTQLQVSYTPQLQDLPLAQEHTDSEGEPEEPSTTLV 480
Db 421 LQEEVSTQGTLLESQAALAVLGPTQLQVSYTPQLQDLPLAQEHTDSEGEPEEPSTTLV 480

Qy 481 DWDPTQRLCTIPSLSSFDQSEGCPEBGDLGBEGLLSRLYEBPADPPRPPGENETVIMQ 540
Db 481 DWDPTQRLCTIPSLSSFDQSEGCPEBGDLGBEGLLSRLYEBPADPPRPPGENETVIMQ 540

Qy 541 FMEEWGLYVQMEN 553
Db 541 FMEEWGLYVQMEN 553

RESULT 13
US-08-943-087-36
; Sequence 36, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:

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; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-943-087-40

Query Match      100.0%; Score 2947; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.6e-267;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRAPGRPALRPLPLPLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLTQTPPE 60
Db      1 MRAPGRPALRPLPLPLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLTQTPPE 60

QY      61 GLOGVKVTVTVQYFIYGOKKWLKSECRNINRTYCDLSAETSDYEHQYAKVKAIWGTKC 120
Db      61 GLOGVKVTVTVQYFIYGOKKWLKSECRNINRTYCDLSAETSDYEHQYAKVKAIWGTKC 120

QY      121 SKWAESGRFPFLETOIGPPEVALTTDEKSIISVLTAPKWKKNPEDLPVSMQOIYSNLK 180
Db      121 SKWAESGRFPFLETOIGPPEVALTTDEKSIISVLTAPKWKKNPEDLPVSMQOIYSNLK 180

QY      181 YNVSVLNTRKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRRAPQSEKQCARTL 240
Db      181 YNVSVLNTRKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRRAPQSEKQCARTL 240

QY      241 KQOSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILYGNEDKRF 300
Db      241 KQOSSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGEKHPANLILYGNEDKRF 300

QY      301 FVPAEKIVINFINISDDSKI SHQDMSLLGKSSDVSSSLNDPOPSGNLRPPQSEEEVXHL 360
Db      301 FVPAEKIVINFINISDDSKI SHQDMSLLGKSSDVSSSLNDPOPSGNLRPPQSEEEVXHL 360

QY      361 GYASHLMEIFCDSEENTEGTSFTQESLSRTIPDKTVIEYDYVRTTIDICAGPEQELS 420
Db      361 GYASHLMEIFCDSEENTEGTSFTQESLSRTIPDKTVIEYDYVRTTIDICAGPEQELS 420

QY      421 LQEVSTQGTLLSQAALAVLGPTLOYSTPQLQDLPLAQEHTDSEEGPEEPSTTLV 480
Db      421 LQEVSTQGTLLSQAALAVLGPTLOYSTPQLQDLPLAQEHTDSEEGPEEPSTTLV 480

QY      481 DWDPTQGLRCIPSLSSFDQSECEPSEGGGLGEGLLSRLYEPPADPPGNETYLMQ 540
Db      481 DWDPTQGLRCIPSLSSFDQSECEPSEGGGLGEGLLSRLYEPPADPPGNETYLMQ 540

QY      541 FMEEWGLYQVMEN 553
Db      541 FMEEWGLYQVMEN 553

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Search completed: April 5, 2006, 11:43:00
Job time : 43.8831 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 5, 2006, 11:29:48 ; Search time 117.705 Seconds

(without alignments)
1160.927 Million cell updates/sec

Title: US-09-745-792A-14

Perfect score: 1644

Sequence: 1 MQFTFWLSEIWTSLFWFF.....VDACATVMSPELLRAWIS 311

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Genesecp1980s.*
2: Genesecp1990s.*
3: Genesecp2000s.*
4: Genesecp2001s.*
5: Genesecp2002s.*
6: Genesecp2003as.*
7: Genesecp2003bs.*
8: Genesecp2004s.*
9: Genesecp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1644	100.0	311	2 AAY41736	Aay41736 Human PRO
2	1644	100.0	311	3 AAY66676	Aay66676 Membrane-
3	1644	100.0	311	3 AAB33440	Aab33440 Human PRO
4	1644	100.0	311	3 AAY44664	Aay44664 Interfero
5	1644	100.0	311	3 AAB44292	Aab44292 Human PRO
6	1644	100.0	311	3 AAY97046	Aay97046 Human TAN
7	1644	100.0	311	4 AAU12187	Aau12187 Human PRO
8	1644	100.0	311	4 AAB85270	Aab85270 Human IL-
9	1644	100.0	311	4 AAE00339	Aae00339 Human cyt
10	1644	100.0	311	4 AAU04059	Aau04059 Human int
11	1644	100.0	311	4 AAB65199	Aab65199 Human PRO
12	1644	100.0	311	5 ABG67201	Abg67201 Human int
13	1644	100.0	311	5 ABB90182	Abb90182 Human pol
14	1644	100.0	311	5 AAE23355	Aae23355 Human int
15	1644	100.0	311	5 ABB84877	Abb84877 Human PRO
16	1644	100.0	311	5 AAE29064	Aae29064 Human IL-
17	1644	100.0	311	5 ABB95483	Abb95483 Human ang
18	1644	100.0	311	6 ABUS8014	Abus8014 Human PRO
19	1644	100.0	311	6 ABUS59092	Abus59092 Novel hum
20	1644	100.0	311	6 ABUS2604	Abus2604 Human sec
21	1644	100.0	311	6 ABO17631	Abol7631 Novel hum
22	1644	100.0	311	6 ABUS0523	Abus0523 Human sec
23	1644	100.0	311	6 ABO25238	Abos25238 Novel hum
24	1644	100.0	311	6 ABO13905	Abol13905 Human PRO

ALIGNMENTS

RESULT 1

AA41736
ID AAY41736 standard; protein; 311 AA.

XX AAY41736;

XX DT 07-DEC-1999 (first entry)

XX DE Human PRO1114 protein sequence.

XX KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein.

XX OS Homo sapiens.

XX PN WO9946281-A2.

XX PD 16-SEP-1999.

XX PF 08-MAR-1999; 99WO-US005028.

XX PR 10-MAR-1998; 98US-0077450P.

XX PR 11-MAR-1998; 98US-0077632P.

XX PR 11-MAR-1998; 98US-0077641P.

XX PR 12-MAR-1998; 98US-0077649P.

XX PR 13-MAR-1998; 98US-0077791P.

XX PR 17-MAR-1998; 98US-0078004P.

XX PR 20-MAR-1998; 98US-0004020.

XX PR 20-MAR-1998; 98US-0078866P.

XX PR 20-MAR-1998; 98US-0078910P.

XX PR 20-MAR-1998; 98US-0078936P.

XX PR 25-MAR-1998; 98US-0078939P.

XX PR 25-MAR-1998; 98US-0079294P.

XX PR 26-MAR-1998; 98US-0079556P.

XX PR 27-MAR-1998; 98US-0079663P.

XX PR 27-MAR-1998; 98US-0079664P.

XX PR 27-MAR-1998; 98US-0079689P.

XX PR 27-MAR-1998; 98US-0079728P.

XX PR 27-MAR-1998; 98US-0079786P.

XX PR 30-MAR-1998; 98US-0079920P.

XX PR 30-MAR-1998; 98US-0079923P.

XX PR 31-MAR-1998; 98US-0080105P.

XX PR 31-MAR-1998; 98US-0080107P.

XX PR 31-MAR-1998; 98US-0080165P.

XX PR 31-MAR-1998; 98US-0080194P.

XX PR 01-APR-1998; 98US-0080327P.

XX PR 10-MAR-1998; 98US-0077450P.

XX PR 11-MAR-1998; 98US-0077632P.

XX PR 11-MAR-1998; 98US-0077641P.

XX PR 12-MAR-1998; 98US-0077649P.

XX PR 13-MAR-1998; 98US-0077791P.

XX PR 17-MAR-1998; 98US-0078004P.

XX PR 20-MAR-1998; 98US-0004020.

XX PR 20-MAR-1998; 98US-0078866P.

XX PR 20-MAR-1998; 98US-0078910P.

XX PR 20-MAR-1998; 98US-0078936P.

XX PR 25-MAR-1998; 98US-0078939P.

XX PR 25-MAR-1998; 98US-0079294P.

XX PR 26-MAR-1998; 98US-0079556P.

XX PR 27-MAR-1998; 98US-0079663P.

XX PR 27-MAR-1998; 98US-0079664P.

XX PR 27-MAR-1998; 98US-0079689P.

XX PR 27-MAR-1998; 98US-0079728P.

XX PR 27-MAR-1998; 98US-0079786P.

XX PR 30-MAR-1998; 98US-0079920P.

XX PR 30-MAR-1998; 98US-0079923P.

XX PR 31-MAR-1998; 98US-0080105P.

XX PR 31-MAR-1998; 98US-0080107P.

XX PR 31-MAR-1998; 98US-0080165P.

XX PR 31-MAR-1998; 98US-0080194P.

XX PR 01-APR-1998; 98US-0080327P.

PR 01-APR-1998; 98US-0080328P.
PR 01-APR-1998; 98US-0080333P.
PR 01-APR-1998; 98US-0080334P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
PR 09-APR-1998; 98US-0081195P.
PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0081952P.
PR 15-APR-1998; 98US-0081955P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082767P.
PR 23-APR-1998; 98US-0082796P.
PR 27-APR-1998; 98US-0083336P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083392P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083500P.
PR 29-APR-1998; 98US-0083545P.
PR 29-APR-1998; 98US-0083554P.
PR 29-APR-1998; 98US-0083558P.
PR 29-APR-1998; 98US-0083559P.
PR 30-APR-1998; 98US-0083742P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084441P.
PR 07-MAY-1998; 98US-0084598P.
PR 07-MAY-1998; 98US-0084600P.
PR 07-MAY-1998; 98US-0084627P.
PR 07-MAY-1998; 98US-0084837P.
PR 07-MAY-1998; 98US-0084839P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 13-MAY-1998; 98US-0085323P.
PR 13-MAY-1998; 98US-0085338P.
PR 13-MAY-1998; 98US-0085339P.
PR 15-MAY-1998; 98US-0085573P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085689P.
PR 15-MAY-1998; 98US-0085697P.
PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0085704P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
XX (GETH) GENENTECH INC.
XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX WPI; 1999-551358/46.
XX N-PSDB; AA234190.
XX New secreted and transmembrane polypeptides and their polynucleotides,
XX useful for treating blood coagulation disorders, cancers and cellular

PT adhesion disorders.
XX Claim 12; Fig 142; 530pp; English.
XX The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as sources
CC of probes, primers, for chromosome mapping, and for generation of
CC antisense sequences. They can also be used to create transgenic animals.
CC The proteins can be used to treat a variety of diseases and disorders,
CC depending on their function. Diseases that may be treated include blood
CC coagulation disorders, cancers and cellular adhesion disorders. They may
CC also be used to raise antibodies. AA233891 to AA234338, and AA41685 to
CC AA41774 represent polynucleotide and polypeptide sequence given in the
CC exemplification of the present invention
XX Sequence 311 AA;
SQ

Query Match 100.0%; Score 1644; DB 2; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.4e-164;
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOTFTWVLEIWTSLFMWFFYALIPCLLTDEVAIIPAPONLSVLSTNMKHLWMSVFIAP 60
|||||
DB 1 MOTFTWVLEIWTSLFMWFFYALIPCLLTDEVAIIPAPONLSVLSTNMKHLWMSVFIAP 60
|||||
QY 61 GETVYVSVEYQGEYSLSYTSHTWIPSSWCSLTEGPECVTDITATVPYNLRVRLTGSQ 120
|||||
DB 61 GETVYVSVEYQGEYSLSYTSHTWIPSSWCSLTEGPECVTDITATVPYNLRVRLTGSQ 120
|||||
QY 121 TSAMSLKHPFNRSITLTPGMEITKOGFHLVIELEDLGPQFEFLVAYVRREPGEAEHV 180
|||||
DB 121 TSAMSLKHPFNRSITLTPGMEITKOGFHLVIELEDLGPQFEFLVAYVRREPGEAEHV 180
|||||
QY 181 KVRSGGIPVHLETWEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPLVLFALF 240
|||||
DB 181 KVRSGGIPVHLETWEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPLVLFALF 240
|||||
QY 241 VGFMLILVVVPLFVWKGRLLOYSCCPVVLPDTLKITNSPOKLISCRREEVDACATVM 300
|||||
DB 241 VGFMLILVVVPLFVWKGRLLOYSCCPVVLPDTLKITNSPOKLISCRREEVDACATVM 300
|||||
QY 301 SPEELLRAWIS 311
|||||
DB 301 SPEELLRAWIS 311
|||||

RESULT 2
AAI66676
ID AAI66676 standard; protein; 311 AA.
XX
AC AAI66676;
XX
XX 05-APR-2000 (first entry)
DT
XX Membrane-bound protein PRO1114.
DE
XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping.
KW
XX Homo sapiens.
OS
XX WO9963088-A2.
PN
XX 09-DEC-1999.
PD
XX 02-JUN-1999; 99WO-US012252.
PF
XX 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.

PR	04-JUN-1998;	98US-00800288
PR	04-JUN-1998;	98US-00800299
PR	04-JUN-1998;	98US-00800309
PR	04-JUN-1998;	98US-00800336
PR	04-JUN-1998;	98US-00800362
PR	05-JUN-1998;	98US-00801679
PR	05-JUN-1998;	98US-00802022
PR	05-JUN-1998;	98US-00802126
PR	05-JUN-1998;	98US-00802179
PR	09-JUN-1998;	98US-00806555
PR	10-JUN-1998;	98US-00807229
PR	10-JUN-1998;	98US-00807302
PR	10-JUN-1998;	98US-00807349
PR	10-JUN-1998;	98US-00807388
PR	10-JUN-1998;	98US-00807409
PR	10-JUN-1998;	98US-00807419
PR	10-JUN-1998;	98US-00807429
PR	10-JUN-1998;	98US-00808610
PR	10-JUN-1998;	98US-00808811
PR	10-JUN-1998;	98US-00808824
PR	10-JUN-1998;	98US-00808825
PR	10-JUN-1998;	98US-00808826
PR	11-JUN-1998;	98US-00808858
PR	11-JUN-1998;	98US-00808861
PR	11-JUN-1998;	98US-00808863
PR	11-JUN-1998;	98US-00808876
PR	12-JUN-1998;	98US-00809090
PR	12-JUN-1998;	98US-00809105
PR	16-JUN-1998;	98US-00809440
PR	16-JUN-1998;	98US-00809512
PR	17-JUN-1998;	98US-00809514
PR	17-JUN-1998;	98US-00809532
PR	17-JUN-1998;	98US-00809538
PR	17-JUN-1998;	98US-00809598
PR	17-JUN-1998;	98US-00809599
PR	17-JUN-1998;	98US-00809600
PR	17-JUN-1998;	98US-00809653
PR	18-JUN-1998;	98US-00809801
PR	18-JUN-1998;	98US-00809307
PR	18-JUN-1998;	98US-00809308
PR	19-JUN-1998;	98US-00809479
PR	19-JUN-1998;	98US-00809488
PR	22-JUN-1998;	98US-00809522
PR	22-JUN-1998;	98US-00902466
PR	22-JUN-1998;	98US-00902529
PR	22-JUN-1998;	98US-00902549
PR	23-JUN-1998;	98US-00903499
PR	23-JUN-1998;	98US-00903555
PR	24-JUN-1998;	98US-00904299
PR	24-JUN-1998;	98US-00904319
PR	24-JUN-1998;	98US-00904355
PR	24-JUN-1998;	98US-00904449
PR	24-JUN-1998;	98US-00904455
PR	24-JUN-1998;	98US-00904619
PR	24-JUN-1998;	98US-00904729
PR	25-JUN-1998;	98US-00905355
PR	25-JUN-1998;	98US-00905389
PR	25-JUN-1998;	98US-00905409
PR	25-JUN-1998;	98US-00905579
PR	25-JUN-1998;	98US-00906769
PR	25-JUN-1998;	98US-00906789
PR	25-JUN-1998;	98US-00906889
PR	25-JUN-1998;	98US-00906909
PR	25-JUN-1998;	98US-00908919
PR	25-JUN-1998;	98US-00908949
PR	25-JUN-1998;	98US-00908959
PR	25-JUN-1998;	98US-00908969
PR	25-JUN-1998;	98US-00908963
PR	01-JUL-1998;	98US-00913589
PR	01-JUL-1998;	98US-00913609
PR	02-JUL-1998;	98US-00914789
PR	02-JUL-1998;	98US-00914869

(GETH) GENENTECH INC.

Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
Wood WI, Yuan J;

WPI; 2000-072883/06.
N-PSDB; AAZ65011.

Membrane-bound proteins and related nucleotide sequences.

Claim 12: Fig 117: 822pp: English.

The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO

CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC also be useful for the preparation of PRO polypeptides, especially by
CC recombinant techniques
CC
CC
CC Sequence 311 AA;
SQ

Query Match	100.0%;	Score 1644;	DB 3;	Length 311;
Best Local Similarity	100.0%;	Pred. No. 1.4e-164;		
Matches 311;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MQFTMWLEELWTSLFWMFFFYALIPCLLTDBVAILPAPONLSVLSTNNKHLLMWSPIAP	60	
Db	1	MQFTMWLEELWTSLFWMFFFYALIPCLLTDBVAILPAPONLSVLSTNNKHLLMWSPIAP	60	
Qy	61	GETVYVSEYQGEYESLYTSHIWIPSSWCSLTEGPCDVTDDITATVPYNLRVRATLGSQ	120	
Db	61	GETVYVSEYQGEYESLYTSHIWIPSSWCSLTEGPCDVTDDITATVPYNLRVRATLGSQ	120	
Qy	121	TSAWSILKHPFNRRNSTILTRPGMEITKDGPHLVLTLEDLGQPFELVAYWRERPGAEHV	180	
Db	121	TSAWSILKHPFNRRNSTILTRPGMEITKDGPHLVLTLEDLGQPFELVAYWRERPGAEHV	180	
Qy	181	KWVRSGGIPVHLETMPEGAAVCVKAQTFVKAIGRYSAFSQTECVVEQGEATPLVALPAF	240	
Db	181	KWVRSGGIPVHLETMPEGAAVCVKAQTFVKAIGRYSAFSQTECVVEQGEATPLVALPAF	240	
Qy	241	VGFMILLVWVPLFWKMGRLQYSCCPPVVLPTLKITNSPQKLISCRREEVDCATAVM	300	
Db	241	VGFMILLVWVPLFWKMGRLQYSCCPPVVLPTLKITNSPQKLISCRREEVDCATAVM	300	
Qy	301	SPEELLRAWIS	311	
Db	301	SPEELLRAWIS	311	

RESULT 3
AAB33440
ID AAB33440 standard; protein; 311 AA.
XX
XX AAB33440;
XX AC
XX AC
XX DT 29-JAN-2001 (first entry)
XX DE Human PRO1114 protein UNQ557 SEQ ID NO:144

Human; immune related disease; diagnosis; antiinflammatory; cardiac;
dermatological; antiarthritic; antirheumatic; immunosuppressive;
haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
antinaeamic; hepatotropic; virucide; antipsoriatic; antiallergic;
antisthmatic; systemic lupus erythematosus; rheumatoid arthritis;
osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
autoimmune thrombocytopaenia; immune-mediated renal disease;
demyelinating disease; hepatobiliary disease; Whipple's disease;
inflammatory bowel disease; gluten-sensitive enteropathy;
autoimmune disease; immune-mediated skin disease; allergic disease;
immunological disease; transplantation associated disease;
graft rejection; graft-versus-host-disease.

XX	Homo sapiens.
OS	
XX	WO200053758-A2.
PN	
XX	14-SEP-2000.
PD	

XX	02-MAR-2000	2000WO-US005841.1
PF		
XX		
PR	08-MAR-1999	99WO-US0050268.
PR	10-MAR-1999	99US-1236181P.
PR	12-MAR-1999	99US-1239575P.
PR	23-MAR-1999	99US-0125775P.
PR	13-APR-1999	99US-0128849P.
PR	20-APR-1999	99WO-US00861S.
PR	28-APR-1999	99US-0134445P.
PR	04-MAY-1999	99US-0132371P.
PR	14-MAY-1999	99US-0134287P.
PR	22-JUN-1999	99WO-US01012S.
PR	20-JUL-1999	99US-0141037P.
PR	28-JUL-1999	99US-0144758P.
PR	28-JUL-1999	99US-0145698P.
PR	01-SEP-1999	99US-0146222P.
PR	08-SEP-1999	99WO-US020111.
PR	11-SEP-1999	99WO-US020594.
PR	13-SEP-1999	99WO-US020944.
PR	15-SEP-1999	99WO-US021090.
PR	15-SEP-1999	99WO-US021547.
PR	29-OCT-1999	99WO-US023089.
PR	29-OCT-1999	99US-0162506P.
PR	30-NOV-1999	99WO-US028214.
PR	30-NOV-1999	99WO-US028313.
PR	30-NOV-1999	99WO-US028409.
PR	01-DEC-1999	99WO-US028301.
PR	01-DEC-1999	99WO-US028634.
PR	02-DEC-1999	99WO-US028551.
PR	02-DEC-1999	99WO-US028564.
PR	02-DEC-1999	99WO-US028565.
PR	16-DEC-1999	99WO-US03009S.
PR	20-DEC-1999	99WO-US030999.
PR	30-DEC-1999	99WO-US031274.
PR	06-JAN-2000	2000WO-US000219.
PR	06-JAN-2000	2000WO-US000277.
PR	08-JAN-2000	2000WO-US000376.
PR	11-FEB-2000	2000WO-US00356S.
PR	11-FEB-2000	2000WO-US004341.
PR	18-FEB-2000	2000WO-US004342.
PR	22-FEB-2000	2000WO-US004414.
PR	22-FEB-2000	2000WO-US004414.

(GETH) GENENTECH INC.

Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;

WPI; 2000-572271/53.
N-PSDB: AAC58605.

Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.

Claim 33: Fig 54; 309pp; English.

The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases, allergic diseases, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease. AAC58397 to AAC59578

CC represent PCR primers and hybridisation probes used in the isolation of
CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
CC represent human PRO polynucleotide and protein sequences given in the
CC exemplification of the present invention
XX
XX
SQ Sequence 311 AA;

Query Match 100.0%; Score 1644; DB 3; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.4e-164;
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQFTTWLEIWTSLFMWFFYALIPCLLTDEVAIPAPQNLVSLTNMKHLLMWSPIAP 60
DB 1 MQFTTWLEIWTSLFMWFFYALIPCLLTDEVAIPAPQNLVSLTNMKHLLMWSPIAP 60

QY 61 GETVYVSVEYQGEYESLYTSHIWPSSWCSLTGPECDVTDITATVPYNLVRATLGSQ 120
DB 61 GETVYVSVEYQGEYESLYTSHIWPSSWCSLTGPECDVTDITATVPYNLVRATLGSQ 120

QY 121 TSAWSILKHPFNNSITLTPGMEITKDGPHLVIELEDLGPOFEFLVAYWRREPGEAEHV 180
DB 121 TSAWSILKHPFNNSITLTPGMEITKDGPHLVIELEDLGPOFEFLVAYWRREPGEAEHV 180

QY 181 KMVRSGGIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECEVQGEAIPLVLFALFAF 240
DB 181 KMVRSGGIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECEVQGEAIPLVLFALFAF 240

QY 241 VGFMLILVVVPLFVWKMGRLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATVM 300
DB 241 VGFMLILVVVPLFVWKMGRLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATVM 300

QY 301 SPEELLRAWIS 311
DB 301 SPEELLRAWIS 311

RESULT 4
AAY44664
ID AAY44664 standard; protein; 311 AA.
AC AAY44664;
XX
XX
DT 18-APR-2000 (first entry)
DE Interferon Receptor-HKAEF92.
XX
KW Interferon receptor HKAEF92; INFR; ATCC No. 209746; viral infection;
KW immune dysfunction; immune system disorder; proliferative disease;
KW cancer; inflammatory disorder; persistent infection; autoimmune disease;
KW arthritis; leukemia; lymphoma; immunosuppression; myelosuppression;
KW inflammatory bowel disease; Jaks-STATS signal transduction pathway;
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Signal_peptide
FT Peptide 69..77
FT /note= "Antigenic epitope-bearing peptide"
FT Peptide 92..107
FT /note= "Antigenic epitope-bearing peptide"
FT Peptide 129..162
FT /note= "Antigenic epitope-bearing peptide"
FT Domain 130..233
FT /label= Extracellular_domain
FT Peptide 172..199
FT /note= "Antigenic epitope-bearing peptide"
FT Domain 234..250
FT /label= Transmembrane_domain
FT Domain 251..311
FT /label= Intracellular_domain
FT Peptide 272..307
FT /note= "Antigenic epitope-bearing peptide"

XX WO9962934-A1.
XX PD 09-DEC-1999.
XX PF 03-JUN-1999; 99WO-US012156.
XX PR 05-JUN-1998; 98US-0088185P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Ruben SM, Ni J;
XX WPI; 2000-147043/13.
XX N-PSDB; AA249747.
XX New isolated interferon receptor HKAEF92 polynucleotides, used to develop
XX products for treating, e.g. immune system related disorders.
XX Claim 17; Fig 1; 98pp; English.
XX
CC The present sequence is interferon receptor (INFR) HKAEF92 encoded by
CC cDNA clone HKAEF92 (ATCC No. 209746) derived from human keratinocyte cDNA
CC library. INFR-HKAEF92 polypeptides are used in the treatment of disorders
CC associated with viral infection, immune dysfunction and proliferative
CC diseases such as cancer, inflammatory disorders, persistent infection,
CC autoimmune diseases, arthritis, leukemias, lymphomas, immunosuppression,
CC inflammatory bowel disease, or myelosuppression. The products can also be
CC used for detection, diagnosis and drug screening. INFR-HKAEF92 protein
CC activates Jaks-STATS signal transduction pathway in a dose-dependent
XX manner
XX
SQ Sequence 311 AA;

Query Match 100.0%; Score 1644; DB 3; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.4e-164;
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQFTTWLEIWTSLFMWFFYALIPCLLTDEVAIPAPQNLVSLTNMKHLLMWSPIAP 60
DB 1 MQFTTWLEIWTSLFMWFFYALIPCLLTDEVAIPAPQNLVSLTNMKHLLMWSPIAP 60

QY 61 GETVYVSVEYQGEYESLYTSHIWPSSWCSLTGPECDVTDITATVPYNLVRATLGSQ 120
DB 61 GETVYVSVEYQGEYESLYTSHIWPSSWCSLTGPECDVTDITATVPYNLVRATLGSQ 120

QY 121 TSAWSILKHPFNNSITLTPGMEITKDGPHLVIELEDLGPOFEFLVAYWRREPGEAEHV 180
DB 121 TSAWSILKHPFNNSITLTPGMEITKDGPHLVIELEDLGPOFEFLVAYWRREPGEAEHV 180

QY 181 KMVRSGGIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECEVQGEAIPLVLFALFAF 240
DB 181 KMVRSGGIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECEVQGEAIPLVLFALFAF 240

QY 241 VGFMLILVVVPLFVWKMGRLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATVM 300
DB 241 VGFMLILVVVPLFVWKMGRLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATVM 300

QY 301 SPEELLRAWIS 311
DB 301 SPEELLRAWIS 311

RESULT 5
AAB44292
ID AAB44292 standard; protein; 311 AA.
XX AAB44292;
XX
DT 08-FEB-2001 (first entry)
DE Human PRO1114 (UNQ557) protein sequence SEQ ID NO:352.
XX

CC 242 genes have been localized to human chromosomes 1p36 and 3q21,
CC respectively. The proteins, cDNA and their modulators can be used for the
CC treatment of viral and bacterial infection, inflammatory and autoimmune
CC disorders, vascular injury and inhibition of angiogenesis. In particular,
CC TANGO 241 can be used to treat pancreatic disorders and TANGO 242 can be
CC used to treat brain disorders
XX
SQ Sequence 311 AA;

Query Match 100.0%; Score 1644; DB 3; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.4e-164;
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQFTFWLVEEITWTSIFMWFYALIPCLLTDEVAIIPAPQNLVLTNMKHLNWSVVIAP 60
DB 1 MQFTFWLVEEITWTSIFMWFYALIPCLLTDEVAIIPAPQNLVLTNMKHLNWSVVIAP 60

QY 61 GETVYVSVEYQGEYSLYTSIHWIPSWCSLTPGECVTDVDDITATVPYNLRVATLGSQ 120
DB 61 GETVYVSVEYQGEYSLYTSIHWIPSWCSLTPGECVTDVDDITATVPYNLRVATLGSQ 120

QY 121 TSAMSLKHPFNRRNSTILTRPGMEITKDGPHLVIELEDLGPQFEFLVAYWRREPGEAEHV 180
DB 121 TSAMSLKHPFNRRNSTILTRPGMEITKDGPHLVIELEDLGPQFEFLVAYWRREPGEAEHV 180

QY 181 KMRVSGGIPVHLETPMFGAAYCVKAQTFVKAIGRYSAFSGTECVQGEAIPVLVLFAP 240
DB 181 KMRVSGGIPVHLETPMFGAAYCVKAQTFVKAIGRYSAFSGTECVQGEAIPVLVLFAP 240

QY 241 VGFMLTLVVVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEDVACATVM 300
DB 241 VGFMLTLVVVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEDVACATVM 300

QY 301 SPEELLRAWIS 311
DB 301 SPEELLRAWIS 311

RESULT 7
AAU12187
ID AAU12187 standard; protein; 311 AA.
XX
AC AAU12187;
XX
XX 24-OCT-2001 (first entry)
DT
XX Human PRO1114 polypeptide sequence.
DE
XX Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW A-peptide; factor VIIA; gene therapy.
XX
XX Homo sapiens.
XX
XX WO200140466-A2.
PN
XX 07-JUN-2001.
XX
XX 01-DEC-2000; 2000WO-US032678.
XX
XX 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 05-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
XX

(GETH) GENENTECH INC.
PA
XX Baker KP, Beresini M, Deforge L, Deenovers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2001-408281/43.
DR N-PSDB; AAS21259.
XX
XX Isolated , secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT breast, prostate, cervical.
XX
XX Claim 12; Fig 32; 813pp; English.
XX
XX AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
CC polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO
CC polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 275 sequences are also useful to stimulate the release of tumour
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC differentiation of chondrocytes, the proliferation or gene expression in
CC pericyte cells, the release of proteoglycans from cartilage, the
CC proliferation of inner ear utricular supporting cells or of T-
CC lymphocytes, the release of a cytokine from peripheral blood monocytes
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC VIIA. The PRO polypeptides can be used in assays to identify molecules
CC involved in binding interactions. The polynucleotides encoding PRO
CC polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy
XX
SQ Sequence 311 AA;

Query Match 100.0%; Score 1644; DB 4; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.4e-164;
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQFTFWLVEEITWTSIFMWFYALIPCLLTDEVAIIPAPQNLVLTNMKHLNWSVVIAP 60
|||||

Db 1 MOTFTMWLEIWTSLPMFFYALIPCLLTDEVAIIPAPQNLSVLSTNMKHLMMSPVIAP 60
QY 61 GETVYYSVEYQGEYSLYTSHIWIPSWCSLSTEGPECDVTDITATVPYNLRVRAITLGSQ 120
Db 61 GETVYYSVEYQGEYSLYTSHIWIPSWCSLSTEGPECDVTDITATVPYNLRVRAITLGSQ 120
QY 121 TSAMSIKHPFNRSNTILTRPGMEITKDGFLHVLIELEDLGPQEFVLVYWRREPGEAEHV 180
Db 121 TSAMSIKHPFNRSNTILTRPGMEITKDGFLHVLIELEDLGPQEFVLVYWRREPGEAEHV 180
QY 181 KMYRSGGIPVHLETMPEGAAAYCVKAQTFVKAIGRYSAFSQTECEVEQGEAIPLVLAIFAF 240
Db 181 KMYRSGGIPVHLETMPEGAAAYCVKAQTFVKAIGRYSAFSQTECEVEQGEAIPLVLAIFAF 240
QY 241 VGFMLILVVVPLFVWKMGRLLOYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATVM 300
Db 241 VGFMLILVVVPLFVWKMGRLLOYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATVM 300
QY 301 SPEELLRAWIS 311
Db 301 SPEELLRAWIS 311
RESULT 8
AAB85270
ID AAB85270 standard; protein; 311 AA.
XX AAB85270;
XX AAB85270;
DT 07-SEP-2001 (first entry)
XX Human IL-20 receptor subunit IL-20RB.
DE Interleukin 20; IL-20; IL-20RA; Zcytor7; IL-20RB; DIRS1; immunoglobulin;
KW antinflammatory; antipsoriatic; antiasthmatic; antibacterial; human;
KW dermatological; antiulcer; antagonist.
XX Homo sapiens.
XX WO200146232-A2.
XX 28-JUN-2001.
XX 22-DEC-2000; 2000WO-US035307.
XX 23-DEC-1999; 99US-00471774.
XX 22-JUN-2000; 2000US-0213416P.
XX (ZYMO) ZYMOGENETICS INC.
XX Foster DC, Xu W, Madden KL, Kelly JD, Sprecher CA, Brandt CS;
PI Rixon MW, Preenell SR, Fox BA,
XX WPI; 2001-398320/42.
DR N-PSDB; AAH22816.
XX Isolated interleukin 20 soluble receptor comprising two polypeptide
PT subunits IL-20RA and IL-20RB, useful for down-regulating IL-20 and thus
PT treating inflammatory diseases such as psoriasis.
XX Example 2; Page 68-69; 119pp; English.
XX The invention relates to an interleukin 20 (IL-20) soluble receptor
CC comprising two polypeptide subunits IL-20RA (formerly known as Zcytor7)
CC and IL-20RB (formerly known as DIRS1). The two subunits are preferably
CC linked together, in one embodiment, one subunit is fused to the constant
CC region of the light chain of an immunoglobulin, and the other subunit is
CC fused to constant region of the heavy chain of an immunoglobulin. The
CC light chain and the heavy chain are connected via a disulphide bond. The
CC soluble receptor can be used to down-regulate IL-20 and thus treat
CC inflammatory diseases such as psoriasis, inflammatory lung injury such as
CC asthma or bronchitis, adult respiratory disease (ARD), septic shock,
CC multiple organ failure, bacterial pneumonia, eczema, atopic and contact

CC dermatitis, and inflammatory bowel disease such as ulcerative colitis and
CC Crohn's disease. The present sequence represents a human IL-20 receptor
CC subunit IL-20RB
XX Sequence 311 AA;
SQ Query Match 100.0%; Score 1644; DB 4; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.4e-164;
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MOTFTMWLEIWTSLPMFFYALIPCLLTDEVAIIPAPQNLSVLSTNMKHLMMSPVIAP 60
Db 1 MOTFTMWLEIWTSLPMFFYALIPCLLTDEVAIIPAPQNLSVLSTNMKHLMMSPVIAP 60
QY 61 GETVYYSVEYQGEYSLYTSHIWIPSWCSLSTEGPECDVTDITATVPYNLRVRAITLGSQ 120
Db 61 GETVYYSVEYQGEYSLYTSHIWIPSWCSLSTEGPECDVTDITATVPYNLRVRAITLGSQ 120
QY 121 TSAMSIKHPFNRSNTILTRPGMEITKDGFLHVLIELEDLGPQEFVLVYWRREPGEAEHV 180
Db 121 TSAMSIKHPFNRSNTILTRPGMEITKDGFLHVLIELEDLGPQEFVLVYWRREPGEAEHV 180
QY 181 KMYRSGGIPVHLETMPEGAAAYCVKAQTFVKAIGRYSAFSQTECEVEQGEAIPLVLAIFAF 240
Db 181 KMYRSGGIPVHLETMPEGAAAYCVKAQTFVKAIGRYSAFSQTECEVEQGEAIPLVLAIFAF 240
QY 241 VGFMLILVVVPLFVWKMGRLLOYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATVM 300
Db 241 VGFMLILVVVPLFVWKMGRLLOYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATVM 300
QY 301 SPEELLRAWIS 311
Db 301 SPEELLRAWIS 311
RESULT 9
AAE00339
ID AAE00339 standard; protein; 311 AA.
XX AAE00339;
XX AAE00339;
DT 19-JUN-2001 (first entry)
XX Human cytokine receptor protein, CG92.
DE Human; cytokine receptor protein; CG92; antiinflammatory; antimicrobial;
KW immunosuppressive; blood coagulation disorder; antidiabetic; cytostatic;
KW gastrointestinal; acute pancreatitis; glomerulonephritis; gene therapy;
KW severe combined immunodeficiency; SCID; autoimmune disorder; thrombosis;
KW multiple sclerosis; rheumatoid arthritis; Alzheimer's disease; xenograft;
KW graft versus host disease; GVHD; inflammatory bowel disease; haemostatic;
KW endotoxin shock; psoriasis; osteoporosis; hepatitis; vascular; allograft;
KW cell proliferative; haematopoietic; vasculitis; lupus; leukaemia; cancer;
KW sarcoidosis; sepsis.
XX Homo sapiens.
OS Key Location/Qualifiers
FH Key 1..29 /label= Signal_peptide
FT Peptide 30..311
FT Protein /label= Mature_human.CG92_protein
FT Region 35..224 /note= "Tissue factor structure region"
FT Region 39..157 /label= Tissue_factor_signature
FT Region 40..226 /note= "Tissue factor structure region"
FT Domain 84..119 /label= Tissue_factor_domain
FT Region 235..255 /note= "Shows high homology to bacterial chemotaxis
FT sensory transducer signature"

Db 1 MQTFTMWLBEIWTSLFMWFFYALIPCLLTDEVAIIPAPQNLVSLTNMKHLLMWSPIAP 60
QY 61 GETVYYSVEYQGEYESLYTSHIWPSSWCSLTEGPECDVTDITATVPYNLRVRATLGSQ 120
Db 61 GETVYYSVEYQGEYESLYTSHIWPSSWCSLTEGPECDVTDITATVPYNLRVRATLGSQ 120
QY 121 TSAMWSILKHPFNNSITLTPGMEITKDGFLHVLIELEDLGPQFEFLVAYWRREPGEAEHV 180
Db 121 TSAMWSILKHPFNNSITLTPGMEITKDGFLHVLIELEDLGPQFEFLVAYWRREPGEAEHV 180
QY 181 KMWRSGGIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSGTECVQGEAIPLVLALFAP 240
Db 181 KMWRSGGIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSGTECVQGEAIPLVLALFAP 240
QY 241 VGFMLILVVVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPOKLI SCRREEDVACATAYM 300
Db 241 VGFMLILVVVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPOKLI SCRREEDVACATAYM 300
QY 301 SPEELLRAWIS 311
Db 301 SPEELLRAWIS 311
RESULT 11
AAB65199
ID AAB65199 standard; protein; 311 AA.
XX AAB65199;
AC AAB65199;
XX
DT 02-APR-2001 (first entry)
TX Human PRO1114 (UNQ557) protein sequence SEQ ID NO:183.
DE Human
XX Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
KW cancer; chromosomal mapping; Gene mapping; tissue typing;
KW diagnostic assay.
XX Homo sapiens.
OS
XX WO2000073454-A1.
PN
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US008439.
XX
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US005884.
PR 20-MAR-2000; 2000WO-US007377.
XX
XX (GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Deanoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX WPI; 2001-032160/04.
DR N-PSDB; AAF44157.
XX
PT PRO polynucleotides used to produce polypeptides used to target bioactive
PT molecules such as toxins, radiolabels or antibodies, to specific cells,
PT to cause targeted cell death.
XX
PS Claim 12; Fig 117; 935pp; English.
XX
CC The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can
CC be used for targeted delivery of bioactive molecules, such as toxins,
CC radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
CC DNA. They may also be used to produce transgenic animals which are used
CC to develop and screen therapeutically useful reagents. The PRO nucleotide
CC and protein sequence can be used for tissue typing and in treating
CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
CC AAF44470 represent PCR primers and hybridisation probes used in the
CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
CC AAB65300 represent human PRO polynucleotide and protein sequences given
CC in the exemplification of the present invention
XX
SQ Sequence 311 AA;
Query Match 100.0%; Score 1644; DB 4; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.4e-164;
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQTFTMWLBEIWTSLFMWFFYALIPCLLTDEVAIIPAPQNLVSLTNMKHLLMWSPIAP 60
Db 1 MQTFTMWLBEIWTSLFMWFFYALIPCLLTDEVAIIPAPQNLVSLTNMKHLLMWSPIAP 60
QY 61 GETVYYSVEYQGEYESLYTSHIWPSSWCSLTEGPECDVTDITATVPYNLRVRATLGSQ 120
Db 61 GETVYYSVEYQGEYESLYTSHIWPSSWCSLTEGPECDVTDITATVPYNLRVRATLGSQ 120
QY 121 TSAMWSILKHPFNNSITLTPGMEITKDGFLHVLIELEDLGPQFEFLVAYWRREPGEAEHV 180
Db 121 TSAMWSILKHPFNNSITLTPGMEITKDGFLHVLIELEDLGPQFEFLVAYWRREPGEAEHV 180
QY 181 KMWRSGGIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSGTECVQGEAIPLVLALFAP 240
Db 181 KMWRSGGIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSGTECVQGEAIPLVLALFAP 240
QY 241 VGFMLILVVVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPOKLI SCRREEDVACATAYM 300
Db 241 VGFMLILVVVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPOKLI SCRREEDVACATAYM 300
QY 301 SPEELLRAWIS 311
Db 301 SPEELLRAWIS 311
RESULT 12
ABG67201
ID ABG67201 standard; protein; 311 AA.
XX
AC ABG67201;
XX
DT 24-SEP-2002 (first entry)
XX
DE Human interleukin-20 sub-unit IL20RB.
XX
KW Inflammation; interleukin-20; IL-20; interleukin-8; IL-8; chemokine;
KW neutrophil; monocyte; basophil; eosinophil; chemoattractant; psoriasis;

periodontal disease; rheumatoid arthritis; idiopathic pulmonary fibrosis; angiogenesis-dependent chronic inflammatory condition; lung cancer; melanoma; inflammatory disease; diabetes; arteriosclerosis; cataract; reperfusion injury; cancer; meningitis; rheumatic disease; skin disease; idiopathic pulmonary fibrosis; inflammatory bowel disease; psoriasis; ulcerative colitis; eczema; atopic dermatitis; contact dermatitis; inflammatory lung disease; ARD; adult respiratory disease; asthma; bronchitis; pneumonia.

OS Homo sapiens.

XX US2002042366-A1.

XX 11-APR-2002.

XX 22-DEC-2000; 2000US-00746359.

XX 23-DEC-1999; 99US-0171969P.

PR 22-JUN-2000; 2000US-0213341P.

XX (THOM/) THOMPSON P.

PA (POST/) FOSTER D C.

PA (XUW/) XU W.

PA (MADD/) MADDEN K L.

PA (KELL/) KELLY J D.

PA (SPRE/) SPRECHER C A.

PA (BLUM/) BLUMBERG H.

PA (BAGA/) BAGAN M A.

PA (JASP/) JASPERS S R.

PA (CHAN/) CHANDRASEKHER Y A.

PA (NOVA/) NOVAK J E.

XX Thompson P, Foster DC, Xu W, Madden KL, Kelly JD, Sprecher CA; Blumberg H, Bagan MA, Jaspers SR, Chandrasekher YA, Novak JE; PI

PI WPI: 2002-507215/54.

XX N-PSDB; ABK96177.

XX

XX Treating inflammatory skin and lung diseases using antibodies against interleukins (IL)-20 (which indirectly modulates activation of IL-8), PT useful for treating e.g. psoriasis, asthma and bronchitis.

XX

PS Example 2; Page 23-24; 68pp; English.

XX

XX The invention describes a method (I) for treating a mammal afflicted with a disease in which an interleukin-20 (IL-20) polypeptide plays a role CC comprising administering antagonist of the IL-20 polypeptide to the CC individual. An important cytokine in the inflammatory process is CC interleukin-8 (IL-8), a chemokine that acts as an agonist for neutrophils CC via chemotaxis and the release of granule enzymes. IL-8 binds to CC receptors on neutrophils, monocytes, basophils, and eosinophils. IL-8 is CC a potent chemoattractant for neutrophils; and the early stages of CC periodontal disease are characterized by the influx of neutrophils. IL-8 CC is a potent inducer of angiogenesis in several angiogenesis-dependent CC chronic inflammatory conditions, including rheumatoid arthritis, CC psoriasis, and idiopathic pulmonary fibrosis. Additionally, IL-8 is an CC important source of angiogenic activity in human lung cancer. Also, IL-8 CC expression correlates with experimental metastatic activity of some CC melanoma cell lines. Therefore an effective method to treat inflammatory CC diseases would be to administer an agent that would inhibit IL-8. It has CC been shown that IL-20 up-regulates IL-8. Therefore antagonists to IL-20 CC can be used to treat these diseases. The method is used for treating CC diseases in which the IL-20 polypeptide plays a role e.g. inflammatory CC diseases including diabetes, arteriosclerosis, cataracts, reperfusion CC injury, cancer, meningitis, rheumatic diseases, idiopathic pulmonary CC fibrosis, inflammatory bowel disease (ulcerative colitis), skin disease CC (psoriasis, eczema, atopic dermatitis and contact dermatitis) or an CC inflammatory lung disease (adult respiratory disease (ARD), asthma, CC bronchitis and pneumonia). This sequence represents a human interleukin- CC 20 (IL-20) polypeptide used in developing the method of the invention CC

XX Sequence 311 AA;

Query Match 100.0%; Score 1644; DB 5; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.4e-164;
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQTFTWVLEBIWTSLEPMFFYALIPCLLTDEVAIPAPQNLVSLTNMKHLLMWSPIAP 60
DB 1 MQTFTWVLEBIWTSLEPMFFYALIPCLLTDEVAIPAPQNLVSLTNMKHLLMWSPIAP 60

QY 61 GETVYYSVEYQGEYESLYTSHIWPSSWCSLTGSPCEDVTDITATVPYNLRVRATIGSQ 120
DB 61 GETVYYSVEYQGEYESLYTSHIWPSSWCSLTGSPCEDVTDITATVPYNLRVRATIGSQ 120

QY 121 TSAWSILKHPPFNENSTILTRPGMEITKDGPHLVEILEDLGQFEFLVAYWRREPGEAEHV 180
DB 121 TSAWSILKHPPFNENSTILTRPGMEITKDGPHLVEILEDLGQFEFLVAYWRREPGEAEHV 180

QY 181 KMYRSGGIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSAFSAFSAFSAFSAFSAFSAF 240
DB 181 KMYRSGGIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSAFSAFSAFSAFSAFSAFSAF 240

QY 241 VGFMLILVVVPLFVWKMGRLLOYSCCPVVVLPDTLKITNSPQKLISCRREEVDAATAVM 300
DB 241 VGFMLILVVVPLFVWKMGRLLOYSCCPVVVLPDTLKITNSPQKLISCRREEVDAATAVM 300

QY 301 SPEELLRAWIS 311
DB 301 SPEELLRAWIS 311

RESULT 13
ABB90182
ID ABB90182 standard; protein; 311 AA.
XX
AC ABB90182;
XX
DT 24-MAY-2002 (first entry)
XX
DE Human polypeptide SEQ ID NO 2558.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anti-ulcer; vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.
XX
OS Homo sapiens.
XX
PN WO200190304-A2.
XX
PD 29-NOV-2001.
XX
PF 19-MAY-2001; 2001WO-US016450.
XX
PR 19-MAY-2000; 2000US-0205515P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
DR WPI: 2002-122018/16.
XX N-PSDB; ABL90591.
XX
PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders.
XX
PS Claim 11; SEQ ID NO 2558; 2081pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB9040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are CC isolated from a range of human tissues disclosed in the specification.

CC	The nucleic acids, proteins, antibodies and (ant)agonists are useful in	PD	21-MAR-2002.
CC	the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and	XX	
CC	ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,	PF	13-SEP-2001; 2001WO-US028557.
CC	breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune	XX	
CC	disorders e.g. Addison's disease, allergies, autoimmune haemolytic	PR	15-SEP-2000; 2000US-0233305P.
CC	anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,	XX	(ZYMO) ZYMOGENETICS INC.
CC	multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)	XX	Chandrasekher YA, Jaspers SR;
CC	cardiovascular disorders such as myocardial ischaemias; (d) wound healing	XX	WPI; 2002-425815/45.
CC	; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)	DR	N-PSDB; AAD37555.
CC	infectious diseases such as viral, bacterial, fungal and parasitic	XX	
CC	infections. Note: The sequence data for this patent did not form part of	PT	Method of down-regulating IL-19 useful for treating inflammation
CC	the WIPO specification, but was obtained in electronic format directly	PT	comprises administration of a polypeptide comprised of the extracellular
CC	from Wipo at ftp.wipo.int/pub/published_pct_sequences	PT	domain of IL-20RA and IL-20RB.
XX		XX	
SQ	Sequence 311 AA;	XX	
		PS	Disclosure; Page 50-51; 80pp; English.
		XX	
		CC	The present invention relates to a method of down-regulating interleukin
		CC	(IL)-19. The method involves administration of a polypeptide comprised of
		CC	the extracellular domain of interleukin-20 receptor alpha (IL-20RA) and
		CC	the extracellular domain of interleukin-20 receptor beta (IL-20RB). The
		CC	IL-20RA and IL-20RB are heterodimeric receptors that bind to both IL-19
		CC	and mda7. The method is useful for down-regulating IL-19, useful for the
		CC	treatment of inflammation e.g., in diabetes, atherosclerosis, cataracts,
		CC	reperfusion injury, cancer, infectious meningitis, rheumatoid arthritis,
		CC	rheumatic fever and systemic lupus erythematosus. The present sequence is
		CC	human IL-20RB variant (V-IL-20RB) protein
		XX	
		SQ	Sequence 311 AA;
			Query Match 100.0%; Score 1644; DB 5; Length 311;
			Best Local Similarity 100.0%; Pred. No. 1.4e-164;
			Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MQFTFWLVEEITWTSLFWMFFYALIPCLLTDEVAILLPAPQNLVSLTNMKHLLMWSPIAP 60	QY	1 MQFTFWLVEEITWTSLFWMFFYALIPCLLTDEVAILLPAPQNLVSLTNMKHLLMWSPIAP 60
Db	1 MQFTFWLVEEITWTSLFWMFFYALIPCLLTDEVAILLPAPQNLVSLTNMKHLLMWSPIAP 60	Db	1 MQFTFWLVEEITWTSLFWMFFYALIPCLLTDEVAILLPAPQNLVSLTNMKHLLMWSPIAP 60
QY	61 GETVYYSVEYQGEYESLYTSHIWPSSWCSLTEGPECVTDITATVPYNLRVRATLGSQ 120	QY	61 GETVYYSVEYQGEYESLYTSHIWPSSWCSLTEGPECVTDITATVPYNLRVRATLGSQ 120
Db	61 GETVYYSVEYQGEYESLYTSHIWPSSWCSLTEGPECVTDITATVPYNLRVRATLGSQ 120	Db	61 GETVYYSVEYQGEYESLYTSHIWPSSWCSLTEGPECVTDITATVPYNLRVRATLGSQ 120
QY	121 TSAWSILKHPFNNSITLRPGMEITKDGPHLVIELEDLGPQEFVLVYWRREPGEAEHV 180	QY	121 TSAWSILKHPFNNSITLRPGMEITKDGPHLVIELEDLGPQEFVLVYWRREPGEAEHV 180
Db	121 TSAWSILKHPFNNSITLRPGMEITKDGPHLVIELEDLGPQEFVLVYWRREPGEAEHV 180	Db	121 TSAWSILKHPFNNSITLRPGMEITKDGPHLVIELEDLGPQEFVLVYWRREPGEAEHV 180
QY	181 KMYRSGGIPVHLETPGGAAYCVKAQTFVKAIGRYSAFSQTECVQGEBAIPLVLALFAF 240	QY	181 KMYRSGGIPVHLETPGGAAYCVKAQTFVKAIGRYSAFSQTECVQGEBAIPLVLALFAF 240
Db	181 KMYRSGGIPVHLETPGGAAYCVKAQTFVKAIGRYSAFSQTECVQGEBAIPLVLALFAF 240	Db	181 KMYRSGGIPVHLETPGGAAYCVKAQTFVKAIGRYSAFSQTECVQGEBAIPLVLALFAF 240
QY	241 VGFMILILVVVPLFVWKMGRLQYSCCPVVVLPDTLKITNSPKLIISCRREEVDACATVM 300	QY	241 VGFMILILVVVPLFVWKMGRLQYSCCPVVVLPDTLKITNSPKLIISCRREEVDACATVM 300
Db	241 VGFMILILVVVPLFVWKMGRLQYSCCPVVVLPDTLKITNSPKLIISCRREEVDACATVM 300	Db	241 VGFMILILVVVPLFVWKMGRLQYSCCPVVVLPDTLKITNSPKLIISCRREEVDACATVM 300
QY	301 SPEELLRAWIS 311	QY	301 SPEELLRAWIS 311
Db	301 SPEELLRAWIS 311	Db	301 SPEELLRAWIS 311
			RESULT 15
			ABB84877
ID	AAE23355 standard; protein; 311 AA.	ID	ABB84877 standard; protein; 311 AA.
XX		XX	
AC	AAE23355;	AC	ABB84877;
XX		XX	
DT	27-AUG-2002 (first entry)	DT	16-MAY-2002 (first entry)
XX		XX	
DE	Human interleukin-20 receptor beta variant (V-IL-20RB) protein.	DE	Human PRO1114 protein sequence SEQ ID NO:122.
XX		XX	
KW	Human; interleukin-19; IL-19; interleukin-20 receptor alpha; IL-20RA;	KW	Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
KW	interleukin-20 receptor beta; IL-20RB; inflammation; atherosclerosis;	KW	vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW	diabetes; reperfusion injury; cancer; infectious meningitis; cataract;		
KW	rheumatoid arthritis; rheumatic fever; systemic lupus erythematosus;		
KW	antibacterial; cytostatic; dermatological; ophthalmological; vasotropic;		
KW	variant.		
XX			
OS	Homo sapiens.		
OS	Synthetic.		
XX			
FH	Key Location/Qualifiers		
FT	Peptide 1..29		
FT	/label= Signal_peptide		
FT	30..311		
FT	/note= "Human mature V-IL-20RB protein"		
XX			
PN	WO200222153-A2.		
XX			

KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW age-related macular degeneration; arterial restenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumor angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping.
XX
OS Homo sapiens.

XX

PN W020020690-A2.

XX 03-JAN-2002.

XX 20-JUN-2001; 2001WO-US019692.

XX 23-JUN-2000; 2000US-0213637P.

PR 20-JUL-2000; 2000US-0219556P.

PR 25-JUL-2000; 2000US-0220624P.

PR 25-JUL-2000; 2000US-0220664P.

PR 28-JUL-2000; 2000WO-US020710.

PR 02-AUG-2000; 2000US-0222695P.

PR 17-AUG-2000; 2000US-02243657.

PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.

PR 07-SEP-2000; 2000US-0230978P.

PR 18-SEP-2000; 2000US-02664610.

PR 18-SEP-2000; 2000US-00665350.

PR 24-OCT-2000; 2000US-0242922P.

PR 08-NOV-2000; 2000US-00709238.

PR 08-NOV-2000; 2000WO-US030952.

PR 10-NOV-2000; 2000WO-US030873.

PR 01-DEC-2000; 2000WO-US032678.

PR 20-DEC-2000; 2000US-00747259.

PR 20-DEC-2000; 2000WO-US034956.

PR 22-JAN-2001; 2001US-00767609.

PR 28-FEB-2001; 2001US-00796498.

PR 28-FEB-2001; 2001WO-US006520.

PR 01-MAR-2001; 2001WO-US008666.

PR 09-MAR-2001; 2001US-00802706.

PR 14-MAR-2001; 2001US-00808689.

PR 22-MAR-2001; 2001US-00816744.

PR 05-APR-2001; 2001US-00828366.

PR 10-MAY-2001; 2001US-00854208.

PR 10-MAY-2001; 2001US-00854280.

PR 25-MAY-2001; 2001US-00866028.

PR 25-MAY-2001; 2001US-00866034.

PR 30-MAY-2001; 2001WO-US017092.

PR 30-MAY-2001; 2001US-00870574.

PR 30-MAY-2001; 2001WO-US017443.

PR 01-JUN-2001; 2001WO-US017800.

(GETH) GENENTECH INC.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;

PI Godowski PJ, Gurney AL, Hillan KJ, Marters SA, Pan J, Paoni NF;

PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

XX WPI; 2002-090516/12.

DR N-PSDB; ABL88132.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,

PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial

PT infarction), endothelial or angiogenic disorders in a mammal.

XX Claim 11; Fig 122; 565pp; English.

XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to

CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,

CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic

CC activities, and can be used in gene therapy. The PRO polynucleotides,

CC proteins, agonists and antagonists are useful for treating or diagnosing

CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.

CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,

CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The PRO polynucleotides have applications in molecular biology,
CC including use as hybridisation probes, and in chromosome and gene
CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
CC exemplification of the present invention
XX
SQ Sequence 311 AA;

Query Match

Best Local Similarity 100.0%; Score 1644; DB 5; Length 311;

Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQTFTMVLBEIWTSLFMWFFYALIPCLLTDEVAAILPAPQNLSQLSTNMKHLMLWSPVIAP 60

Db 1 MQTFTMVLBEIWTSLFMWFFYALIPCLLTDEVAAILPAPQNLSQLSTNMKHLMLWSPVIAP 60

QY 61 GETVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITATVPYNLVRATLGSQ 120

Db 61 GETVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITATVPYNLVRATLGSQ 120

QY 121 TSAMSLIKHPFNRNSTILTRPGMEITKDGFLHVLIELEDLGQPEFLVAYWRREPGEAEHV 180

Db 121 TSAMSLIKHPFNRNSTILTRPGMEITKDGFLHVLIELEDLGQPEFLVAYWRREPGEAEHV 180

QY 181 KMYRSGGIPVHLETPMEPGAAYCVKAQTFVKAIGRYSAFQTECVQGEAIPVLALFAF 240

Db 181 KMYRSGGIPVHLETPMEPGAAYCVKAQTFVKAIGRYSAFQTECVQGEAIPVLALFAF 240

QY 241 VGFMLILVVVPLFVWKMGRLLQYSCCPVVLPDTLKITNSPKLISCRREEVDACATVM 300

Db 241 VGFMLILVVVPLFVWKMGRLLQYSCCPVVLPDTLKITNSPKLISCRREEVDACATVM 300

QY 301 SPEELLRAWIS 311

Db 301 SPEELLRAWIS 311

Search completed: April 5, 2006, 11:35:37

Job time : 121.705 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: April 5, 2006, 11:36:04 ; Search time 18.3576 Seconds
(without alignments)
1630.025 Million cell updates/sec

Title: US-09-745-792A-14
Perfect score: 1644
Sequence: 1 MTFYVLEIWTSLFMWFF.....VDACATVMSPELLRAWIS 311

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: Pirl:*
2: Pirl:*
3: Pirl:*
4: Pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	204	12.4	325	2 A47003	Cytokine receptor
2	189.5	11.5	590	2 A45283	interferon alpha/b
3	188.5	11.5	337	2 I38500	interferon gamma r
4	183.5	11.2	349	2 JC6311	interferon recepto
5	181.5	11.0	560	2 S27387	interferon alpha r
6	173.5	10.6	557	2 A32694	interferon gamma r
7	163	9.9	332	2 A49947	interferon gamma r
8	148	9.0	578	2 I56215	interleukin-10 rec
9	139	8.5	292	1 KFRB3	tissue factor prec
10	132.5	8.1	295	1 KFHU3	tissue factor prec
11	129.5	7.9	575	2 A49667	interleukin-10 rec
12	126.5	7.7	294	1 KFM53	tissue factor prec
13	122	7.4	489	2 A31555	interferon gamma r
14	117.5	7.1	292	1 KFB03	tissue factor prec
15	111	6.8	507	1 A32385	erythropoietin rec
16	103.5	6.3	1118	1 A49724	protein-tyrosine-p
17	101.5	6.2	419	2 T10652	hypothetical prote
18	96	5.8	507	1 A46713	erythropoietin rec
19	96	5.8	984	2 A39753	protein-tyrosine k
20	95	5.8	896	2 I56563	interleukin-3 rece
21	94.5	5.7	359	2 S55653	hypothetical prote
22	94	5.7	508	1 ZUHR	erythropoietin rec
23	93.5	5.7	1427	2 I51669	tumor suppressor -
24	93	5.7	1447	2 A54100	tumor suppressor p
25	92	5.6	379	2 S56193	probable membrane
26	92	5.6	977	2 S49044	tyrosine kinase Mp
27	92	5.6	2311	1 TVCHSR	kinase-related pro
28	91.5	5.6	987	2 A54092	protein-tyrosine k
29	89.5	5.4	567	2 F81682	phosphoenolpyruvat

30 89 5.4 985 2 I51549 receptor tyrosine
31 87.5 5.3 896 1 A35782 cytokine receptor
32 87.5 5.3 1328 2 JS0610 beta-galactosidase
33 87 5.3 831 2 JQ1655 prolactin receptor
34 87 5.3 952 2 I50612 protein-tyrosine k
35 86 5.2 227 2 I37081 cytochrome-c oxida
36 86 5.2 227 2 T11483 cytochrome-c oxida
37 86 5.2 549 2 S74467 hypothetical prote
38 85.5 5.2 345 2 G87801 protein C10G11.4
39 85.5 5.2 1557 2 D41214 protein-tyrosine-p
40 85.5 5.2 1630 2 C11250 protein-tyrosine-p
41 85 5.2 227 2 T11250 cytochrome-c oxida
42 85 5.2 227 2 T11053 cytochrome-c oxida
43 85 5.2 265 2 S14081 erythropoietin rec
44 85 5.2 495 2 H69614 aldehyde dehydroge
45 84.5 5.1 454 2 T20829 probable serine ca

ALIGNMENTS

RESULT 1

A47003
Cytokine receptor family class II protein CRF2-4 precursor - human
C:Species: Homo sapiens (man)
C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C:Accession: A47003, G01418
R:Lutalla, G.; Gardiner, K.; Uze, G.
Genomics 16, 366-373, 1993
A>Title: A new member of the cytokine receptor gene family maps on chromosome 21 at less
A:Reference number: A47003; MUID:93300510; PMID:8314576
A:Accession: A47003
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-325 <LUT>
A:Cross-references: UNIPROT:Q08334; UNIPARC:UPI0000048F14; GB:Z17227; NID:G3933378; PIDN:
R:Lutalla, G.
Submitted to the EMBL Data Library, April 1994
A:Reference number: G06935
A:Accession: G01418
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-123,'D','125-268,'VGRME','<LU2>
A:Cross-references: UNIPARC:UPI000016A09D; EMBL:U08988; NID:G571295; PID:G571296

Query Match 12.4%; Score 204; DB 2; Length 325;
Best Local Similarity 27.1%; Pred. No. 2.7e-10;
Matches 79; Conservative 47; Mismatches 113; Indels 52; Gaps 17;
QY 12 WTSLFWMFYALICLLTDEVALPAPNLVSLSTNKKHLLMW-SPIAPGEVTVYSVEY 70
DB 3 W-SLGSW-----LGGCLLVSGALGVPPPNVNMVNFKNILQWESPAFARG-----NLTF 52
QY 71 QGEYESLYTSHIWPSSWCSLTGEPDCTDDITATVPYNLRVRATLGSQTSAW-SILKH 129
DB 53 TQAQYLSYR-----IFODKCNMTLTTECDFS-SUSKYGDHFLRVRAFADSHSDWVITFC 106
QY 130 PFNRNSTILTRPGM--EITKDGPHLVIELEDLGPQFE-----FLVAYWR 171
DB 107 PV--DDTIIGPGCMQVEVLADSLH-----MRFAPKIENEYETWTMKNVNSWTYVQYWK 160
QY 172 RFGAEHVHVMVRSGGIPVHLETMPEGAAYCVQAQFVFAIGRYSAFSQTECV-VOGEA 230
DB 161 N--GTDEKQITPOYDFEV-LRNLEPWTTCVQVRGFLPDRNKAGSEWSPVCQTTHDET 217
QY 231 IP---LVTLALFAFVGFMJLVVVPLF--VYKMGRLQYSCCPVVLPTLTK 276

C:Accession: JC6311
R:Gibbs, V.C.; Pennica, D.
Gene 186, 97-101, 1997
A:Title: CRF2-4: isolation of cDNA clones encoding the human and mouse proteins.
A:Reference number: JC6311; MUID:97199375; PMID:90477351

A:Accession: JC6311
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-349 <GB>
A:Cross-references: UNIPROT:Q8VHM7; UNIPARC:UPI000017C6DE; GB:U53696

Query Match 11.2%; Score 183.5; DB 2; Length 349;
Best Local Similarity 23.7%; Pred. No. 1.9e-08;
Matches 68; Conservative 49; Mismatches 117; Indels 53; Gaps 13;

QY 23 LIPG-----LLTDEVAIPAPQNLVLSTNMKHLMLMSPVIAGETVYYSVEYQGEY 74

DB 1 MAPCVAGLGGFLVLPALGMIPPEKVRMNSVNFKNILQWEVPAFPKTNLTFTAQYE-SY 59

QY 75 ESIYTSHTIPSSWCSLITGPECVDVDDITATVPYNLRVRATLGSQTSAM-SILKHPPNR 133

DB 60 RS-FQDH-----CKRTASTQCDFS-HUSKYGDYTVRRAELADEHSEWNVTFPCV-- 108

QY 134 NSTILRPGMEITKDGFLHVLIEDLGQPE-----FLVAYWRRBPGAE 177

DB 109 EDTIIGPPEMQI--ESLASLELRFSAPOLENEPETWTLKNIYDSWAYRVQYWK--GTN 164

QY 178 EHVWVRSGGIPVHLETPGGAAYCVKAQTFVKAIGRYSAFSQTCEVQGE----- 229

DB 165 EKQVSVSDSEV-LRNLEPWTTCYIQVQGLDQNRGTGSESPICERTGNDITPSWIV 223

QY 230 APLVLALFAVCFMILLVVPFLVMKGRLLQYSCCPVVLPDTLK 276

DB 224 AILIVSVLVFLFLGCFV---LWLIYKTKHTFRSGTSLPQHLK 267

RESULT 5

S27387
interferon alpha receptor type 1 precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

A:Accession: S27387
R:Mouchel-Vielh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G.
FEBS Lett. 313, 255-259, 1992

A:Title: Specific antiviral activities of the human alpha interferons are determined at F&S Lett. 313, 255-259, 1992

A:Reference number: S27387; MUID:93076908; PMID:1446745

A:Accession: S27387
A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA
A:Residues: 1-560 <MOU>

A:Cross-references: UNIPROT:Q04790; UNIPARC:UPI000012D698; EMBL:X68443; NID:g431; PIDN:Q

A:Experimental source: MDBK cells
R:Lim, J.K.; Langer, J.A.

Biochim. Biophys. Acta 1173, 314-319, 1993

A:Title: Cloning and characterization of a bovine alpha interferon receptor.

A:Reference number: S33770; MUID:93305725; PMID:8318540

A:Accession: S33770
A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA
A:Residues: 1-421, 'V', 423-560 <LIM>

A:Cross-references: UNIPARC:UPI0000167C2D; EMBL:L06320; NID:g163187; PIDN:AAA02571.1; PI

A:Experimental source: lung
C:Keywords: antiviral; cytokine receptor; transmembrane protein

F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-560/Product: interferon alpha receptor type 1 #status predicted <MAT>

Query Match 11.0%; Score 181.5; DB 2; Length 560;

Best Local Similarity 22.9%; Pred. No. 5.2e-08;
Matches 73; Conservative 62; Mismatches 133; Indels 51; Gaps 14;

QY 21 YALIPCLLTDEVAIPAPQNLVLSTNMKHLMLMSPVIAGETVYYSVEYQGEYSILYTS 80

DB 215 YSPVYCINTTHERKVPSPENIQINADNQIYVLKW-----DYPENATFQAWLRAFFK 267

QY 81 HI-----W--IPSSWCSLITGPECVDVDDITATVPYNLRVRATLGSQTSAMSIKHPF 131

DB 268 KIPGNHSDKKWKQIPN--CENVSTHCVFPREVSSRGIIYVVRASNGNGTSSFHSEKEFN 325

QY 132 NRNSTILTRPGM---EITKDGPHLVI-----ELEDLGQV---FEFLVAYWRRBPGAEHV 180

DB 326 TEMKTIIPPPVISVKSVTDDSLHVSVGASESENMSVNQLYPLIYEVIFEWENTSNAERKV 385

QY 181 KWRSGGIPVHLETPGGAAYCVKAQTFVKAIGRY--SAFSQTECEVQV-----GEALPLV 234

DB 386 LEKRTNFI---FPDLKPLTVYCVKARALINDRRNRKGSFSDTVCSEKTPGNTSKTWLIV 442

QY 235 LALFAVFGMLILVVVPLFVMKGRLLQYSCCPVVLPDTLK--ITNSPOK--LISSCRE 290

DB 443 GTCTALFSPVIYVVSVEL---RCVKYVFPSSKPPSSVDVEYFSDQPLRNLLLTSEE 498

QY 291 EVDAC-----ATAVMSPEE 304

DB 499 QTERCFIENASIITEIEE 517

RESULT 6

A32694

interferon alpha/beta receptor precursor - human

C:Species: Homo sapiens (man)

C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004

C:Accession: A32694; S17112

R:Uze, G.; Lutfalla, G.; Gresser, I.

Cell 60, 225-234, 1990

A:Title: Genetic transfer of a functional human interferon alpha receptor into mouse cell

A:Reference number: A32694; MUID:90124632; PMID:2153461

A:Accession: A32694

A:Molecule type: mRNA

A:Residues: 1-557 <UZE>

A:Cross-references: UNIPROT:PI1781; UNIPARC:UPI000002D51B; GB:J03171; NID:g184645; PIDN:J

R:Lutfalla, G.

submitted to the EMBL Data Library, July 1991

A:Description: The structure of the human interferon alpha/beta receptor gene.

A:Reference number: S17112

A:Accession: S17112

A:Molecule type: DNA

A:Residues: 1-16, 'A', 18-329, 'V', 343-557 <LUT>

A:Cross-references: UNIPARC:UPI0000179801; EMBL:X60459; NID:g32671

C:Genetics:

A:Gene: GDB:IFNAR1; IFNAR; IFRC

A:Map position: 21q22.1-21q22.1

A:Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3

C:Keywords: cytokine receptor; glycoprotein; transmembrane protein

F;1-21/Domain: transmembrane #status predicted <TRN1>

F;437-455/Domain: transmembrane #status predicted <TRN2>

F;50,58,81,88,110,172,254,313,314,376,416,433,507,518,537/Binding site: carbohydrate (As

Query Match 10.6%; Score 173.5; DB 2; Length 557;

Best Local Similarity 22.3%; Pred. No. 2.6e-07;

Matches 72; Conservative 55; Mismatches 113; Indels 83; Gaps 17;

QY 21 YALIPCLLTDEVAIPAPQNLVLSTNMKHLMLMSPVIAGETVYYSVEYQGEYSILY- 79

DB 215 YSPVCHIKTTVENELPPENIEVSVQNVVLKW-----DYTYANMTFQVQLHAFK 267

QY 80 -----SHIWPSSWCSLITGPECVDVDDITATVPYN-----LRVRATLGSQTSAM- 125

DB 268 RNPGNHLY---KWKQI---PDCENVKTKTCQFPQNVFQKGIYLLRVQASDGNNTSWSEE 321

QY 126 -----ILKHPENRNSTILTRPGMEITKDGPHLVI-----ELEDGPOFEF 165

DB 322 IKPDTIQIAPLPPPPVFNRS-----LSDSFHYIYGAPKQSGNTPTVIQYDIYE- 370

QY 166 LVAYWRRBPGAEHVWVRSGGIPVHLETPGGAAYCVKAQ--TFVKAIGRYSAFSQTCE 223

DB 371 -IIFWENTSNAERKIIKKT---DVTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSFSAVC 426

```
QY 224 VEQV-GEAIPVLALFAVGFMLILVVVFLVWMKGRLLQYSCCPVVVLPDLTKITNS-- 280
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 427 EKTGNTSKIWL-----IVGICIALFALPPVIAAKVFLR--CINVVFP-SLKRPSSID 479
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 281 -----PQK--LLISCRREEVDAC 295
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 480 EYFSEQFLKNLLSTSEQIEKC 502
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
A49947
interferon gamma receptor beta subunit - mouse
N;Alternate names: IFN-gamma R beta chain; IFN-gamma R species-specific cofactor; type I
C;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
R;Hemmi, S.; Bonni, R.; Stark, G.; Di Marco, F.; Aguet, M.
Cell 76, 803-810, 1994
A;Title: A novel member of the interferon receptor family complements functionality of
A;Reference number: A49947; MUID:94170381; PMID:8124717
A;Accession: A49947
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-332 <HEM>
A;Cross-references: UNIPROT:Q63953; UNIPARC:UPI0000022068; GB:S69336; NID:G545841; PIDN:
A;Experimental source: early B-cell line Y16
A;Note: sequence extracted from NCBI backbone (NCBIN:145654, NCBIP:145656)
C;Keywords: cytokine receptor

Query Match 9.9%; Score 163; DB 2; Length 332;
Best Local Similarity 27.3%; Pred. No. 1.2e-06;
Matches 73; Conservative 34; Mismatches 100; Indels 60; Gaps 17;

QY 17 MNEFFALICLL-----TDEVAIPAPQNLSVLSTNMKHLMSVPVIAPGETVY 66
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6 LW-----LPSLLCGLGAAASPDSFSQLAAPNPRHLNYNDEQILTWEP--SPSSNDPR 58
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 67 SVEYQGEVSLTSHIWPSSWCSLSTEGPEC-DVTD--DITA-----TVPYN--LRV 113
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 PVYQVEYS-----FIDGSHRLLP-NCNCTDIETKCDLGGRLKLPHPFTVFLR 110
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 114 RATLQSQTSAWSILKHPFNRSNTILTRP--GMEITKDGPHLVIELE---DL--GPQFEPL 166
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 111 RAKRGNLTSKWGLE--PFQHYENVTVGPPKNISVTPKGSLSLVTHFSPPDPVHGATFQYL 169
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 167 VAYWRREPOAEHVK-MVRSGGIPVILETMEPGAAYCVKAQTFV-----KAIGRYSAFSQT 221
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 170 VHYWEKSETQEQVEGPFKNSIV--LGNLKPVRVYCLQTEAQLILKNKKIRPHGLLSNV 227
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 222 ECVEVQGEA-----IPLVLALFAPV 241
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 228 SCHETTANASARLQVILLPLGIFALL 254
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
I56215
interleukin-10 receptor - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I56215
R;Liu, Y.; Wei, S.H.; Ho, A.S.; de Waal Malefyt, R.; Moore, K.W.
J. Immunol. 152, 1821-1829, 1994
A;Title: Expression cloning and characterization of a human IL-10 receptor.
A;Reference number: I56215; MUID:194165477; PMID:8120391
A;Accession: I56215
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-578 <RES>
A;Cross-references: UNIPROT:Q13651; UNIPARC:UPI00000012BB; EMBL:U00672; NID:G482802; PID
C;Genetics:
A;Gene: GDB:IL10R; HIL-10R
A;Cross-references: GDB:330958; OMIM:146933
```

```
A;Map position: 11q23.3-11q23.3
C;Superfamily: interleukin-10 receptor IL10R
C;Keywords: cytokine receptor

Query Match 9.0%; Score 148; DB 2; Length 578;
Best Local Similarity 22.7%; Pred. No. 4.9e-05;
Matches 68; Conservative 46; Mismatches 107; Indels 78; Gaps 12;

QY 23 LIPCLLTDEVAJ-----LPAPQNLSVLSTNMKHLMSVPVIAPGETVTVYSVE 69
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MLPCLVLLAALLSLRGLSDAHGTPLPSPSVWFPAEFPHHILHWTPIFNQSESTCYEVA 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 70 YQGEVESLYTSHIWPSSWCSLSTEGPEC-DVTDITATVPYNLRVRATIGSQTSAWSILK 128
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 L-----LRYGIESMNSISNCSQTLSDYDLTAVTLDLVHNSGYRVRVAVDGRSHSNWTVTN 115
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 129 HPFNRSNTILT-----RPGMEITKDGPHLVIELEDLGPQF-EFLV 167
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 116 TRFSDEVTLTVGSVNLEIHNGFILGKIQLPRKMAPANDTY-----ESIFSHFREYEI 169
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 168 AYWRREPG-----AEEHVKVRSGGIPVHLETMEPGAAYCVKAQTFVKAIGRYSAP 218
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 170 AI-RKVPNGFTTHKKVKHENSFLTSGEV-----GEFCVQVKSVAASRNSKGMW 218
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 219 SQTCEVEV--QGEAIPVLALFAFV---GFMLILVVVFLVWMKGRLLQYSCCPVVVL 271
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 219 SKEECISLTRQVTVTNVIIPFAFVLLSGALAYCLALQLYVRRKKL-----PSVLL 271
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
KFRB3
tissue factor precursor - rabbit
N;Alternate names: coagulation factor III
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JU0441; S23681
R;Andrews, B.S.; Rehmtulla, A.; Fowler, B.J.; Edgington, T.S.; Mackman, N.
Gene 98, 265-269, 1991
A;Title: Conservation of tissue factor primary sequence among three mammalian species.
A;Reference number: JU0441; MUID:91200676; PMID:1840552
A;Accession: JU0441
A;Molecule type: mRNA
A;Residues: 1-292 <AND>
A;Cross-references: UNIPROT:P24055; UNIPARC:UPI0000136CA5; GB:M55390; NID:G165696; PIDN:
A;Experimental source: brain
R;Pawashe, A.; Ezekowitz, M.; Lin, T.C.; Horton, R.; Bach, R.; Konigsberg, W.
Thromb. Haemost. 66, 315-320, 1991
A;Title: Molecular cloning, characterization and expression of cDNA for rabbit brain tis
A;Reference number: S23681; MUID:92081032; PMID:1746002
A;Accession: S23681
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 33-292 <PAW>
A;Cross-references: UNIPARC:UPI000016C544; EMBL:X53521; NID:G1495; PIDN:CAA37597.1; PID:
C;Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor f
C;Comment: Expression of tissue factor can be induced in a variety of tissues by certain
C;Superfamily: tissue factor
C;Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane
F;1-32/Domain: signal sequence #status predicted <SIG>
F;33-292/Product: tissue factor #status predicted <MAT>
F;33-249/Domain: extracellular #status predicted <EXT>
F;250-271/Domain: transmembrane #status predicted <EXT>
F;272-292/Domain: intracellular #status predicted <INT>
F;41,114,154,167,182/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;79-87,216-239/Disulfide bonds: #status predicted
F;274/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match 8.5%; Score 139; DB 1; Length 292;
Best Local Similarity 24.8%; Pred. No. 0.00013;
Matches 63; Conservative 34; Mismatches 99; Indels 58; Gaps 11;

QY 40 NLSVLSTNMKHLMSVPVIAPGETVTVYSVYQGEYESLYTSHI-----WIPSSWCSLST 93
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```


Db 41 NLTKSTNFKTILEWEP-----KSIDH-----VYTVQISTRLNWN--KSKCFLTA 83

QY 94 GPCEVDVDDITATV--PYNLRVATGTSQTSAMSILKHPFRNS-----TILTRPGM 143

Db 84 ETECDLTDVVKDVGQTYMARVLVSYPARNGNTTGFPPEPPFRNSPEFTPYLDTNLGOPTI 143

QY 144 E-ITKQGFHLVIELED-----LGPOFEFLVAYWRREPCAEHVKWVRS 185

Db 144 QSEQVGTGLNVTVQDARTLVRNGTFLSLRAVFGKDLNLTLYWR-----ASSTGKKTAT 199

QY 186 GGIPVHLETMPEGAAYCVKAQTFVKAIGR--YSAFSQTECV-EVQGEAIPLVIALFAFVG 242

Db 200 TTNTEFLIDVKGECNYCFYQAVIPSKRRKQRPESILTECTREQGRAREMFFIIGAVV 259

QY 243 FMLILVVVPLFVK 256

Db 260 VALLIIVLSVTYK 273

RESULT 10

KFHU3

tissue factor precursor [validated] - human

N;Alternate names: coagulation factor III

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text change 09-Jul-2004

C;Accession: A43645; A47574; A28320; A29062; A29672; A29008

R;MacKman, N.; Morrissey, J.H.; Fowler, B.; Edgington, T.S.

Biochemistry 28, 1755-1762, 1989

A;Title: Complete sequence of the human tissue factor gene, a highly regulated cellular

A;Reference number: A43645; MUID:89247359; PMID:2719931

A;Accession: A43645

A;Molecule type: DNA

A;Residues: 1-295 <WAC>

A;Cross-references: UNIPARC:UPI000002CD0D; UNIPARC:UPI000002CD0D; GB:J02846; NID:g339505; PIDN:

R;Fisher, K.L.; Gorman, C.M.; Vehar, G.A.; O'Brien, D.P.; Lawn, R.M.

Thromb. Res. 48, 89-99, 1987

A;Title: Cloning and expression of human tissue factor cDNA.

A;Reference number: A47574; MUID:88100453; PMID:3424286

A;Accession: A47574

A;Molecule type: mRNA

A;Residues: 1-295 <FIS>

A;Cross-references: UNIPARC:UPI000002CD0D; GB:M27436; NID:g339507; PIDN:AAA36734.1; PID:

R;Spicer, E.K.; Horton, R.; Bloem, L.; Bach, R.; Williams, K.R.; Guha, A.; Kraus, J.; Li

Proc. Natl. Acad. Sci. U.S.A. 84, 5148-5152, 1987

A;Title: Isolation of cDNA clones coding for human tissue factor: primary structure of t

A;Reference number: A94171; MUID:87260946; PMID:3037536

A;Accession: A28320

A;Molecule type: mRNA

A;Residues: 1-295 <SPI>

A;Cross-references: UNIPARC:UPI000002CD0D; GB:J02931; NID:g339501; PIDN:AAA61150.1; PID:

R;Morrissey, J.H.; Fakhrai, H.; Edgington, T.S.

Cell 50, 129-135, 1987

A;Title: Molecular cloning of the cDNA for tissue factor, the cellular receptor for the

A;Reference number: A29062; MUID:87244317; PMID:3297348

A;Accession: A29062

A;Molecule type: mRNA

A;Residues: 1-295 <MOR>

A;Cross-references: UNIPARC:UPI000002CD0D; GB:J02931; NID:g339501; PIDN:AAA61150.1; PID:

A;Note: part of this sequence, including the amino end of the mature protein, was confir

R;Scarpatti, E.M.; Wen, D.; Broze Jr., G.J.; Miletich, J.P.; Flandermeyer, R.R.; Siegel,

Biochemistry 26, 5234-5238, 1987

A;Title: Human tissue factor: cDNA sequence and chromosome localization of the gene.

A;Reference number: A29672; MUID:88050796; PMID:2823875

A;Accession: A29672

A;Molecule type: mRNA

A;Residues: 1-259, A', 261-295 <SCB>

A;Cross-references: UNIPARC:UPI000004E645; GB:M16553; NID:g339503; PIDN:AAA61151.1; PID:

R;Bach, R.; Konigsberg, W.H.; Nemerson, Y.

Biochemistry 27, 4227-4231, 1988

A;Title: Human tissue factor contains thioester-linked palmitate and stearate on the cyt

A;Reference number: A37422; MUID:89000604; PMID:3166978

A;Contents: annotation; disulfide bonds and fatty acid binding site

C;Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor

C;Comment: Expression of tissue factor can be induced in a variety of tissues by certain

C;Genetics:

A;Gene: GDB:F3

A;Cross-references: GDB:119895; OMIM:134390

A;Map position: 1p22-1p21

A;Introns: 34/1; 71/2; 138/1; 197/3; 251/1

C;Superfamily: tissue factor

C;Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane

F;1-32/Domain: signal sequence #status predicted <SIG>

F;33-295/Product: tissue factor #status experimental <MAT>

F;33-251/Domain: extracellular #status predicted <EXT>

F;252-274/Domain: transmembrane #status predicted <TM>

F;275-295/Domain: intracellular #status predicted <INT>

F;43/Binding site: carboxylate (Asn) (covalent) #status experimental

F;81-89,218-241/Disulfide bonds: #status experimental

F;156,169/Binding site: carboxylate (Asn) (covalent) #status predicted

F;277/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match 8.1%; Score 132.5; DB 1; Length 295;

Best Local Similarity 23.8%; Pred. No. 0.0005;

Matches 64; Conservative 36; Mismatches 120; Indels 49; Gaps 12;

QY 13 TSLFMWFFYALIPCLLTDEVALPAPQNLVSLTNMKHLMWSPVIAPGETVYYSVEYQG 72

Db 19 TLLGLWVFAQVAGASGTTNTV---AAYNLTKSTNFKTILEWEP--KPVNQV-YTVQIST 72

QY 73 EYESLYTSHWIWIPSSWCSLTEGPCDVTDDITATV--PYNLRVATLGSQTSAMSILKHP 130

Db 73 K-----SGDW--KSKCFYTTTECDLTDEIVKDVQTYLARVFSYPAGNVSTGSAGEP 124

QY 131 FNRNS-----TILTRPQME-ITKDGPHLVIELED-----LGPOFE 164

Db 125 LVNSPEFTPYLETNLGQTIQSFQGVTKVNTVDERTLVRNNTFLSLRDVFGKOLI 184

QY 165 FLVAYWRREPGEABEHVKMVRSGSIPVHLETMPEGAAYCVKAQTFV--KAIGRYSAFSQTE 222

Db 185 YTLIYWKSSSSGKTKTAKT---NTNEFLIDVDKGENYCFVSQVAFIPSRVNRKSTDSPVE 240

QY 223 CV-EVQGEAIPLVIALFAFVGFMILIVV 250

Db 241 CMGQEKGEFREIFYIIGAVVVFVILVII 269

RESULT 11

A49667

interleukin-10 receptor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C;Accession: A49667

R;Ho, A.S.; Liu, Y.; Khan, T.A.; Hsu, D.H.; Bazan, J.F.; Moore, K.W.

Proc. Natl. Acad. Sci. U.S.A. 90, 11267-11271, 1993

A;Title: A receptor for interleukin 10 is related to interferon receptors.

A;Reference number: A49667; MUID:94068585; PMID:8248239

A;Accession: A49667

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-575 <RES>

A;Cross-references: UNIPROT:Q61727; UNIPARC:UPI0000023997; GB:L12120; NID:g437615; PIDN:

C;Genetics:

A;Gene: IL10R

C;Superfamily: interleukin-10 receptor IL10R

C;Keywords: cytokine receptor

Query Match 7.9%; Score 129.5; DB 2; Length 575;

Best Local Similarity 20.6%; Pred. No. 0.0021;

Matches 65; Conservative 55; Mismatches 116; Indels 79; Gaps 13;

QY 23 LIPCLLT-----DEVAL---LPAPQNLVSLTNMKHLMWSPVIAPGETVYYSVEYQGE 73

Db 5 LLPFLVTISSLSEFTIAYGTLPSPSYVWFARFQHLFWKFIPIQNSSTSYVEVALK-- 62

QY 74 YESLYTSHWIWIPSSWCSLTEGPCDVT---DDITATVPYNLRVATLGSQTSAMSILKH 129

```
Db 63 ---QYGNSTWNDIHCRAQALSCDLTFTTLDLYHRSYGYRVRVRVAVDNSQYSNWTTTET 119
QY 130 PNRNSTILT-----RPGWEITKQGFHLVIELEDLGPQFELVAY 169
Db 120 RFTVDEVILTVDSVTUKAMGGIYGTIHPRPRITTPAGDEYEQV--FKDL-RVYKISIRK 176
QY 170 WRREPAAEHHVKM-VRSGGIPVHLEMTPEGAAVCVKAQTFVKAIGRYSAFSQTECEVEQG 228
Db 177 FSELKNATKRVKQETFTLTPVIGVR-----KFCVKVLPRLESRIKAEWSEBQCLLIIT 230
QY 229 EAI-----PLVALFAFVGFMILLVVPVLFVWKMGRLLQYSCCPVVVL----- 271
Db 231 EQYFTVTNLISILVISMLLFCG-ILVCLVLQWYIRHPGKL-----PTVLVFRKPHDPFPA 283
QY 272 -----PDTLKITN 279
Db 284 NPLCPETPDIAIHVD 298

RESULT 12
KFW53
tissue factor precursor - mouse
N;Alternate names: coagulation factor III
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A32318; A39046
R;Hartzell, S.; Ryder, K.; Lanahan, A.; Lau, L.F.; Nathans, D.
Mol. Cell. Biol. 9, 2567-2573, 1989
A;Title: A growth factor-responsive gene of murine BALB/c 3T3 cells encodes a protein ho
A;Reference number: A32318; MUID:89343974; PMID:2761539
A;Accession: A32318
A;Molecule type: mRNA
A;Residues: 1-294 <HAR>
A;Cross-references: UNIPROT:P20352; UNIPARC:UPI0000002DD1; GB:M26071; NID:g201924; PIDN:
R;Ranganathan, G.; Blatti, S.P.; Subramaniam, M.; Fae, D.N.; Maible, N.J.; Getz, M.J.
J. Biol. Chem. 266, 496-501, 1991
A;Title: Cloning of murine tissue factor and regulation of gene expression by transformati
A;Reference number: A39046; MUID:91093171; PMID:1985911
A;Accession: A39046
A;Molecule type: mRNA
A;Residues: 1-25,'I',27-294 <RAN>
A;Cross-references: UNIPARC:UPI0000001961; GB:M57896; GB:J05713; NID:g201926; PIDN:AAA63
A;Note: 26-Thr was also found
C;Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
C;Comment: Expression of tissue factor can be induced in a variety of tissues by certain
C;Superfamily: tissue factor
C;Keywords: Blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-294/Product: tissue factor #status predicted <MAT>
F;30-251/Domain: extracellular #status predicted <EXT>
F;252-274/Domain: transmembrane #status predicted <TMW>
F;37,57,169,200/Binding site: carboxylate (Asn) (covalent) #status predicted
F;75-83,218-241/Disulfide bonds: #status predicted
F;275/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match 7.7%; Score 126.5; DB 1; Length 294;
Best Local Similarity 23.7%; Pred. No. 0.0017;
Matches 75; Conservative 41; Mismatches 113; Indels 87; Gaps 17;

QY 22 ALIP-----CLLTDEVAAILPAQ---NLSVLSTNMKHLMWSPVIAPGETVY-YSVEYQGE 73
Db 12 ALAPTFLGCLLLQVTAGAGIPKAFNLTWISTDFKILEWQ-----PKPTNYTYTVQISDR 67
QY 74 YESLYTSHWIWPSWCSLTPGEGCDVDDIT--ATVPYNLRVRATL-----GSQ---- 120
Db 68 -----SRNW--KNKCFSTTDCDLTDEIVKDVWTWAYEAKVLSVPRRNSVHGDGDLVI 119
QY 121 -----TSAWSILKHPRNRSNTILTRPGM-EITKDGFEHLVIELED----- 158
Db 120 HGEPPFTNAPKFLPY-----RDTNLGQPVIOQPEQGRKLNWVVKOSLTLVRKNGTFFTL 175
QY 159 ---LGPQFELVAYWR-RBFGAEHHVKMVRSGGIPVHLEMTPEGAAVC--VKAQTFVKA 212
```

```
Db 176 RQVFGKDLGYIITRYKSGSTGKTKTNTITNTEFSIDV-----BEGVSYCFVQAMIFSRKT 230
QY 213 GRYSAFSQTECEV---VOGEALPLVALFAFVGFMILLVVPVLFVWKMGRLLQYSCCPV 268
Db 231 NQNSPGSSVTCVEQWKSFLGETLIIIVGAVLLATIFILLISLCKRKNRAGQ----- 284
QY 269 VVLPDPTLKITNSPOKL 284
Db 285 -----KGKNTPSRL 293

RESULT 13
A31555
interferon gamma receptor precursor - human
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: A31555
R;Aguet, M.; Dembic, Z.; Merlin, G.
Cell 55, 273-280, 1988
A;Title: Molecular cloning and expression of the human interferon-gamma receptor.
A;Reference number: A31555; MUID:89003065; PMID:2971451
A;Accession: A31555
A;Molecule type: mRNA
A;Residues: 1-489 <AGU>
A;Cross-references: UNIPROT:F15260; UNIPARC:UPI000002CE40; GB:J03143; NID:g184650; PIDN:
C;Genetic:
A;Gene: GDB:IFNGR1; IFNGR
A;Cross-references: GDB:120688; OMIM:107470
A;Map position: 6q23-6q24
C;Superfamily: interferon gamma receptor
C;Keywords: cytokine receptor; transmembrane protein

Query Match 7.4%; Score 122; DB 2; Length 489;
Best Local Similarity 21.2%; Pred. No. 0.0079;
Matches 60; Conservative 54; Mismatches 103; Indels 66; Gaps 12;

QY 35 LPAPQNLSQLSTNMKHLMWSPVIAPGETVY-----YSVEYQGEYSLYTSHWIPSSW 88
Db 29 VPTPTNTVIESYNMNPVIVWYEQIMPQVPVFTVEVKNYGVK-----NSEWIDA-- 76
QY 89 CSLTEGPECDVDDITATVPYN---LRVATIGSQTSAMSLKHPNRSNTILTRPGMEI 145
Db 77 CINIASHHYCNISDHVGD--PSNSLWVRVKARVGQESAYAKSEFAVCRDGKIGPPKLDI 134
QY 146 TKDGFHLVIEL-----EDLGPQFELVAYWR---REPGAEEHVKMVRSG--- 186
Db 135 RKEEKQIMIDIFHPSVFVNGDQEVDDPETTCYIRVNVYVRMNGSEIQYKILTQKEDD 194
QY 187 -----GIPVHLEMTPEGAAVCVKAQTFVKAIGRYSAFSQTECEVEQGEA-----IP 232
Db 195 CDEIQCOLAIPV-----SSLNSQYCVSAEGLVHWGVVTEKSEVCITIFNSSIKGSLWIP 250
QY 233 LVLAIFAFAVGFMILLVVPVLFVWKMGRLLQYSCCPVVVLPTL 275
Db 251 VVAALLLFL--VLSLVFICFYIKKINPLKES-----IILPKSL 287

RESULT 14
KFB03
tissue factor precursor - bovine
N;Alternate names: coagulation factor III
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JQ1319
R;Takayenoki, Y.; Muta, T.; Miyata, T.; Iwanaga, S.
Biochem. Biophys. Res. Commun. 181, 1145-1150, 1991
A;Title: cDNA and amino acid sequences of bovine tissue factor.
A;Reference number: JQ1319; MUID:92109720; PMID:1764065
A;Accession: JQ1319
A;Molecule type: mRNA
A;Residues: 1-292 <TAK>
A;Cross-references: UNIPROT:P30931; UNIPARC:UPI0000136CA3; GB:S74147; NID:g241438; PIDN:
A;Experimental source: adrenal gland
```

A>Note: part of this sequence, including the amino end of the mature protein, was confirmed by the N-terminal amino acid sequence.

C:Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor for tissue factor.

C:Comment: Expression of tissue factor can be induced in a variety of tissues by certain cytokines.

C:Superfamily: tissue factor

C:Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane protein

F:1-35/Domain: signal sequence #status predicted <SIG>

F:36-292/Product: tissue factor #status experimental <MAT>

F:36-248/Domain: extracellular #status predicted <EXT>

F:249-271/Domain: transmembrane #status predicted <TM>

F:272-292/Domain: intracellular #status predicted <INT>

F:43,153,181/Binding site: carboxylate (Asn) (covalent) #status predicted

F:81-89,215-238/Disulfide bonds: #status predicted

F:118,124/Binding site: carboxylate (Thr) (covalent) #status predicted

F:274/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match 7.1%; Score 117.5; DB 1; Length 292;

Best Local Similarity 19.8%; Pred. No. 0.01;

Matches 49; Conservative 41; Mismatches 101; Indels 57; Gaps 9;

Qy 40 NLSVLSTNMKHLMLWSPVIAGETVYYSVEQGEYSLYTSHI-----WIPSSWCSLTE 93

Db 43 NITWKSTNFKTILEWEP-----KPINHVYTVQVISPRLGNW--KMKCFYTT 85

Qy 94 GPECDDVDDITATVPYNLRVLRATLGSQTSAWSILKHPENR-----STILTRPGME-I 145

Db 86 NTECDVTDDEIVKVRRETVLRVLSYPADTSSSTVEPPTNSPEPTPVLETNLGQPTIQSF 145

Qy 146 TKDGFHLVIELED-----LGPOFEFLVAYWRREPGEAEHVMWRSGGI 188

Db 146 EQVGTCLNVTVQDARTLVRANSAPLSLRDVFGRDLNLYYWKASSTGKKKATNTNG-- 203

Qy 189 PVHLETMEPGAAYCVKQAQTFV--KAIGRYSAFSGTECVGEQGEAIPLVLAALPAFVGMPLI 246

Db 204 --FLIVDVKGENYCFHVQAVILSRVNQKSPESPIKTSHEK---VLSTSLFFIIGTVML 258

Qy 247 LVVVPLFV 254

Db 259 VIIIFIV 266

RESULT 15

A32385

erythropoietin receptor precursor, membrane-bound form - mouse

C:Species: Mus musculus (house mouse)

C:Date: 28-Sep-1990 #sequence revision 05-Apr-1995 #text_change 09-Jul-2004

C:Accession: A41686; A32385; S13249

R:Hino, M.; Tojo, A.; Misawa, Y.; Morii, H.; Takaku, F.; Shibuya, M.

Mol. Cell. Biol. 11, 5527-5533, 1991

A:Title: Unregulated expression of the erythropoietin receptor gene caused by insertion

A:Reference number: A41686; MUID:92017832; PMID:1656233

A:Accession: A41686

A:Molecule type: mRNA

A:Residues: 1-507 <HN>

A:Cross-references: UNIPROT:P14753; UNIPARC:UPI000000B997; GB:S59388; NID:g237036; PIDN:

A:Experimental source: murine erythroleukemia (MEL) cell line F5-5

R:D'Andrea, A.D.; Lodish, H.F.; Wong, G.G.

Cell 57, 277-285, 1989

A:Title: Expression cloning of the murine erythropoietin receptor.

A:Reference number: A32385; MUID:89195238; PMID:2539263

A:Accession: A32385

A:Molecule type: mRNA

A:Residues: 1-507 <DAA>

A:Cross-references: UNIPARC:UPI000000B997; GB:J04843; NID:g193090; PIDN:AAA37571.1; PID:

A:Experimental source: murine erythroleukemia (MEL) cells, subclone 745

R:Kuramochi, S.; Ikawa, Y.; Todokoro, K.

J. Mol. Biol. 216, 567-575, 1990

A:Title: Characterization of murine erythropoietin receptor genes.

A:Reference number: S13249; MUID:91080149; PMID:2175360

A:Accession: S13249

A:Molecule type: DNA; mRNA

A:Residues: 1-507 <KUR>

A:Cross-references: UNIPARC:UPI000000B997; EMBL:X53081; NID:g50861; PIDN:CAA37248.1; PID:

A:Experimental source: murine erythroleukemia K-1 cells

```

C:Genetics:
A;Introns: 39/1; 83/2; 142/1; 194/3; 246/1; 275/2; 304/3
C;Superfamily: erythropoietin receptor; cytokine receptor homology
C;Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-507/Product: erythropoietin receptor #status predicted <MAT>
F;25-249/Domain: extracellular #status predicted <EXT>
F;52-238/Domain: cytokine receptor homology <CRS>
F;250-271/Domain: transmembrane #status predicted <TM>
F;272-507/Domain: intracellular #status predicted <INT>
F;52-62,90-106/Disulfide bonds: #status predicted
F;75/Binding site: carbonylate (Asn) (covalent) #status predicted

Query Match          6.8%; Score 111; DB 1; Length 507;
Best Local Similarity 22.5%; Pred. NO. 0.077;
Matches 71; Conservative 41; Mismatches 97; Indels 106; Gaps 18;

Qy 26 CLLTDEVAILLAP-----QNLVSLSTNMKHL--MWSVPIAGETVY 65
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 16 CLLLAGAAWAFSPSLDPKFESKAALLARGSEELLCFTORLEDLVCFEAASSGMDFN 75

Qy 66 YSVRYQGEYSILYTHIWPSSWCSLTEGPE-----CDV--TDDITATVPYNLVRAT 116
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 76 YSFYSQLEGEGRKS-----CSLHQATVRGVSVMWCSLPTADTSSFPVLELQVTEA 126

Qy 117 LGSQTSAWSILKHPNR-----NSTILTRGMEI-----TKDGFHLVIELEDLGPQFEFLVA 168
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 127 SGSPR-----YHRIHIHNEVLLDAPAGLLARRAEEGSHVLR-----164

Qy 169 YWRREPGA--BEHVQWV-----RSGGIPVHLETMEPGAAYCVKQA-----TF-VKA 211
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 165 -WLPPPGAPMTTHIRYEDVDSAGNRAGGTQ-RVEVLE-GRTECVLSNLRGTRITFAVA 221

Qy 212 -----IGRYASQTECVQGEBAIPVLVALFAPVGFMILLVVPFLFWVMG-----R 259
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 222 RMAEPSPSGFWSAWSEPAASLTASDLDPILTL-----SLILVLSLLLTVALLSHRR 275

Qy 260 LLOYSCCPVVLDPDT 274
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 276 TLQOKWPGIFSPES 290
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Search completed: April 5, 2006, 11:41:47
Job time : 20.3576 secs

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Search completed: April 5, 2006, 11:41:47
Job time : 20.3576 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 5, 2006, 11:30:18 ; Search time 110.866 Seconds

(without alignments)
1979.144 Million cell updates/sec

Title: US-09-745-792A-14

Perfect score: 1644

Sequence: 1 MQFTFWLSEIWTSLFWFF.....VDCATAVMSPEELLRAWIS 311

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1644	100.0	311	1 I20RB HUMAN	O6uxl0 homo sapien
2	712	43.3	147	2 Q8IYI5 HUMAN	Q8IYI5 homo sapien
3	265.5	16.1	230	2 Q4TB36 TETNG	Q4TB36 tetraodon n
4	209	12.7	569	2 Q9YHW0 CHICK	Q9YHW0 gallus gall
5	208	12.7	569	2 Q5XPI1 CHICK	Q5XPI1 gallus gall
6	204	12.4	325	1 I10R2 HUMAN	Q08334 homo sapien
7	199.5	12.1	334	2 Q5RL90 CHICK	Q5RL90 gallus gall
8	195.5	11.9	327	2 Q6ZVU9 HUMAN	Q6ZVU9 homo sapien
9	189.5	11.5	590	1 INAR1 MOUSE	F33896 mus musculus
10	188.5	11.5	337	1 INGR2 HUMAN	F38484 homo sapien
11	185.5	11.3	590	2 Q80UR8 MOUSE	Q80UR8 mus musculus
12	183.5	11.2	590	2 Q80UJ3 MOUSE	Q80UJ3 mus musculus
13	182	11.1	449	2 Q5XV05 CHICK	Q5XV05 gallus gall
14	181.5	11.0	349	1 I10R2 MOUSE	Q61190 mus musculus
15	181.5	11.0	560	1 INAR1 BOVIN	Q04790 bos taurus
16	179	10.9	351	2 Q8VHM7 MOUSE	Q8VHM7 mus musculus
17	178.5	10.9	442	2 Q9VJ9 CHICK	Q9VJ9 gallus gall
18	176.5	10.7	477	2 Q4R727 MACFA	Q4R727 macaca fasc
19	175.5	10.7	341	2 Q9YGC8 CHICK	Q9YGC8 gallus gall
20	173.5	10.6	557	1 INAR1 HUMAN	F17181 homo sapien
21	173.5	10.6	557	2 Q53H11 HUMAN	Q53H11 homo sapien
22	173.5	10.6	560	1 INAR1 SHEEP	Q28589 ovis aries
23	172.5	10.5	557	2 Q53GW9 HUMAN	Q53GW9 homo sapien
24	165.5	10.1	305	2 Q6DCU5 XENLA	Q6DCU5 xenopus lae
25	165	10.0	435	2 Q7ZT26 TETNG	Q7ZT26 tetraodon n
26	163.5	9.9	333	2 Q7ZT30 TETNG	Q7ZT30 tetraodon n
27	163.5	9.9	546	1 I20RA MOUSE	Q6phb0 mus musculus
28	163	9.9	332	2 Q78EC1 9MURI	Q78EC1 mus sp. int
29	163	9.9	332	2 Q63953 MOUSE	Q63953 mus musculus
30	160.5	9.8	508	2 Q6QIU4 CHICK	Q6QIU4 gallus gall
31	160.5	9.8	569	2 Q99ND6 RAT	Q99ND6 rattus norv

32	158.5	9.6	508	2 Q9PVK0 CHICK	Q9PVK0 gallus gall
33	155.5	9.5	362	2 Q764M7 PIG	Q764M7 sus scrofa
34	155.5	9.5	508	2 Q9YHV9 CHICK	Q9YHV9 gallus gall
35	155	9.4	553	1 I20RA HUMAN	Q9uhf4 homo sapien
36	154.5	9.4	301	2 Q7ZT35 TETNG	Q7ZT35 tetraodon n
37	154.5	9.4	338	2 Q80UG2 TETNG	Q80UG2 tetraodon n
38	153.5	9.3	317	2 Q58CP3 BOVIN	Q58CP3 bos taurus
39	153	9.3	560	1 INAR1 PIG	Q764m8 sus scrofa
40	151.5	9.2	263	1 I22RA HUMAN	Q969j5 homo sapien
41	151	9.2	345	2 Q4TIA7 TETNG	Q4TIA7 tetraodon n
42	149.5	9.1	213	2 Q8C352 MOUSE	Q8C352 mus musculus
43	148.5	9.0	336	2 Q800E8 TETNG	Q800E8 tetraodon n
44	148	9.0	578	1 I10R1 HUMAN	Q13651 homo sapien
45	140.5	8.5	520	1 I28RA HUMAN	Q8Ius7 h interleuk

ALIGNMENTS

RESULT 1

ID	I20RB_HUMAN	STANDARD;	PRT;	311 AA.
AC	Q6UXL0; Q6P438; Q8TAJ7;			
DT	25-OCT-2004 (Rel. 45, Created)			
DT	25-OCT-2004 (Rel. 45, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Interleukin-20 receptor beta chain precursor (IL-20R-beta) (IL-20R2).			
GN	Name=IL20RB; Synonyms=DIRS1; ORFNames=UNQ557/PRO1114;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).			
RX	MEDLINE=22987309; PubMed=12975309; DOI=10.1101/gr.1293003;			
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,			
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,			
RA	Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,			
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,			
RA	Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,			
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,			
RA	Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,			
RA	Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,			
RA	Wood W.I., Godowski P.J., Gray A.M.;			
RT	"The secreted protein discovery initiative (SPDI), a large-scale			
RT	effort to identify novel human secreted and transmembrane proteins: a			
RT	bioinformatics assessment."			
RL	Genome Res. 13:2265-2270(2003).			
RL	[2]			
RN	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).			
RP	TISSUE=Cervix, and Skin;			
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RX	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Haefl F.,			
RA	Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,			
RA	Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,			
RA	Schmurch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			

[3] PROTEIN SEQUENCE OF 30-44 (ISOFORM 1).
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RL verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
[4]
RP SUBUNIT, LIGAND-BINDING, AND TISSUE SPECIFICITY.
RX MEDLINE=21097717; PubMed=11163236; DOI=10.1016/S0092-8674(01)00187-8;
RA Blumberg H., Conklin D., Xu W.F., Grossmann A., Bender T.,
RA Carollo S., Egan M., Foster D., Haldeman B.A., Hammond A., Haugen H.,
RA Jellinek L., Kelly J.D., Madden K., Maurer M.F., Parrish-Novak J.,
RA Prunkard D., Sexson S., Sprecher C., Waggle K., West J.,
RA Whitmore T.E., Yao L., Kuehle M.K., Dale B.A., Chandrasekhar Y.A.;
RT "Interleukin 20: discovery, receptor identification, and role in
RL epidermal function.";
RL Cell 104:9-19(2001).
[5]
RP SUBUNIT, AND LIGAND-BINDING.
RX PubMed=11564763;
RA Dumoutier L., Leenans C., Lejeune D., Kotenko S.V., Renauld J.-C.;
RT "STAT activation by IL-19, IL-20 and mda-7 through IL-20 receptor
RL complexes of two types.";
RL J. Immunol. 167:3545-3549(2001).
[6]
RP SUBUNIT, AND LIGAND-BINDING.
RX PubMed=12351624; DOI=10.1074/jbc.M205114200;
RA Parrish-Novak J., Xu W., Bender T., Jones C., West J.,
RA Brandt C., Jellinek L., Madden K., McKernan P.A., Foster D.C.,
RA Jaspers S., Chandrasekhar Y.A.;
RT "Interleukins 19, 20, and 24 signal through two distinct receptor
RL complexes: Differences in receptor-ligand interactions mediate unique
RT biological functions.";
RL J. Biol. Chem. 277:47517-47523(2002).
[7]
RP SUBUNIT, AND LIGAND-BINDING.
RX PubMed=14580208; DOI=10.1021/bi0354583;
RA Plotnev S., Magracheva E., Kozlov S., Tobin G., Kotenko S.V.,
RA Wlodawer A., Zdanov A.;
RT "Characterization of the recombinant extracellular domains of human
RL interleukin-20 receptors and their complexes with interleukin-19 and
RL interleukin-20.";
RL Biochemistry 42:12617-12624(2003).
CC -!- FUNCTION: The IL20RA/IL20RB dimer is a receptor for IL19, IL20 and
CC IL24. The IL22RA/IL20RB dimer is a receptor for IL20 and IL24.
CC -!- SUBUNIT: Heterodimer with IL20RA and heterodimer with IL22RA1.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q6UXL0-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q6UXL0-2; Sequence=VSP 011499, VSP 011500;
CC -!- TISSUE SPECIFICITY: Widely expressed with highest levels in skin
CC and testis. Highly expressed in psoriatic skin.
CC -!- SIMILARITY: Belongs to the type II cytokine receptor family.
CC -!- SIMILARITY: Contains 2 fibronectin type-III domains.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AY358305; AAQ08672.1; -; mRNA.
DR EMBL; BC027449; AAH27449.1; -; mRNA.
DR EMBL; BC063696; AAH63696.1; -; mRNA.
DR Ensembl; ENSG00000174564; Homo sapiens.
DR HNCI; HGNC:6004; IL20RB.
DR MIM; 605621; -.
DR InterPro; IPR000282; Cytok receptor_2.
DR InterPro; IPR003961; FN_III.

DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS0853; FN3; 1.
KW Alternative splicing; Direct protein sequencing; Glycoprotein;
KW Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 29 Interleukin-20 receptor beta chain.
FT CHAIN 30 311 Extracellular (Potential).
FT TOPO DOM 30 233 Potential.
FT TRANSMEM 234 254
FT TOPO DOM 255 311
FT DOMAIN 36 137 Cytoplasmic (Potential).
FT DOMAIN 144 228 Fibronectin type-III 1.
FT CARBOHYD 40 40 Fibronectin type-III 2.
FT CARBOHYD 134 134 N-linked (GlcNAc . .) (Potential).
FT DISULFID 202 223 By similarity.
FT VARSPLIC 1 47 Missing (in isoform 2 and isoform 3).
FT VARSPLIC 48 142 /FTID=VSP 011499.
FT VARSPLIC 48 142 Missing (in isoform 2).
FT /FTID=VSP 011500.
SQ SEQUENCE 311 AA; 35076 MW; FF36D518116D9E3 CRC64;
Query Match 100.0%; Score 1644; DB 1; Length 311;
Best Local Similarity 100.0%; Pred. No. 7.6e-136; Indels 0; Gaps 0;
Matches 311; Conservative 0; Mismatches 0;
QY 1 MOTFTWVLEEIWTSLFMWFFYALIPCLLTDEVAIIPAPQNLVSLSTNMKHLMWSPVIAP 60
DB 1 MOTFTWVLEEIWTSLFMWFFYALIPCLLTDEVAIIPAPQNLVSLSTNMKHLMWSPVIAP 60
QY 61 GETVYSVEYQGEYSLSYTHIWISSCSLSTEGPECDDTDDITATVPYNLRVATLGSQ 120
DB 61 GETVYSVEYQGEYSLSYTHIWISSCSLSTEGPECDDTDDITATVPYNLRVATLGSQ 120
QY 121 TSAMSTLKHFPNRSNLTITPCWEITKGFHVLIELELGPQEFVLVAYMRREPGEAEHV 180
DB 121 TSAMSTLKHFPNRSNLTITPCWEITKGFHVLIELELGPQEFVLVAYMRREPGEAEHV 180
QY 181 KMRVSGGIPVHLETMPEGAAYCVKAQTFVKAIGRYSASFQTECVEVQGEAIPLVLALFAF 240
DB 181 KMRVSGGIPVHLETMPEGAAYCVKAQTFVKAIGRYSASFQTECVEVQGEAIPLVLALFAF 240
QY 241 VGFMLILVVVPLFVWKGRLLOYSCCPVVVLPDTTKITNSPKLISCRREEVDACATVM 300
DB 241 VGFMLILVVVPLFVWKGRLLOYSCCPVVVLPDTTKITNSPKLISCRREEVDACATVM 300
QY 301 SPEELLRAWIS 311
DB 301 SPEELLRAWIS 311
RESULT 2
Q8IY5 HUMAN
ID Q8IY5_HUMAN PRELIMINARY; PRT; 147 AA.
AC Q8IY5;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE FNDG6 protein.
GN Name=FNDG6;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore S.I., Wang J., Max S.I., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,

RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Rosa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences.";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN	[2]
RP	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Skin;
RG	NIH WGC Project;
CC	Submitted (JUN-2002) to the EMBL/GenBank/DBSJ databases.
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
DR	EMBL; BC033292; AAH33292.1; -; mRNA.
DR	Ensembl; ENSG00000174564; Homo sapiens.
DR	GO; GO:0016020; C-membrane; IEA.
DR	GO; GO:0004896; P:hematopoietin/interferon-class (D200-domain..); IEA.
DR	InterPro; IPRO00282; CytoK_receptor_2.
KW	Receptor; Transmembrane.
QY	SEQUENCE 147 AA; 16945 MW; 71BAF49274618999 CRC64;
Query Match	43.3%; Score 712; DB 2; Length 147;
Best Local Similarity	100.0%; Pred. No. 2.3e-54;
Matches 131; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	48 MKHLMLMSPVIAPGETYYYSVEYQGYESLYTSHWIPSSWCSLTEGPCVDVTDITATV 107
Db	1 MKHLMLMSPVIAPGETYYYSVEYQGYESLYTSHWIPSSWCSLTEGPCVDVTDITATV 60
QY	108 PYNLVRVATLGQSQTSAWSILKHPPNRNSTILTRPGMEITDKGFHLVIELEDLGPQFFELV 167
Db	61 PYNLVRVATLGQSQTSAWSILKHPPNRNSTILTRPGMEITDKGFHLVIELEDLGPQFFELV 120
QY	168 AYWRERPGAE 178
Db	121 AYWRERPGAE 131
RESULT 3	
Q4TB36_TETNG	
ID	Q4TB36.TETNG PRELIMINARY; PRT; 230 AA.
AC	Q4TB36;
DT	13-SEP-2005 (TrEMBLrel. 31, Created)
DT	13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT	13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE	Chromosome undetermined SCAF7209, whole genome shotgun sequence.
GN	ORFNames=GSTENG0003931001;
OS	Tetradion nigroviridis (Green puffer).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC	Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC	Tetraodontidae; Tetraodontidae; Tetraodon.
OX	NCBI_TaxID=99883;
ON	[1]
RA	NUCLEOTIDE SEQUENCE.
RA	Jallou O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA	Mauceli E., Bouteau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA	Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segreus B.,
RA	Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA	Anthonard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA	Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA	Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA	Parra G., Lardier G., Chapple C., McKernan K.J., Mesirov J.,
RA	Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA	Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA	Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.

[illegible]

Query Match		12.7%; Score 209; DB 2; Length 569;
Best Local Similarity		25.2%; Pred. No. 1.8e-09;
Matches		79; Conservative 52; Mismatches 125; Indels 58; Gaps 14;
QY	21	YALIPCL-LTDEVAIIPAPONLSVLSTNMKHLWSPVAPGTIVYVSVEY-OGEYESLY 78
DB	222	FSPHICIKTRKYNLDLCPNTNRVFPALNMKFFYLWDNHY--NSHVTYTVQVLTGYLKNLY 279
QY	79	T--SHWIPSSWCSLTEGPECDDVTDDITAT-VPYNLRVRATLGSQTSAMS-----125
DB	280	DYSSKQKVGCGENITSMKCNLSVVKPTASYYFRVQAMNEYKSLSKDVEVDPVPT 339
QY	126	-----ILKHPFNRRNSTILTRPGMBITKDGPHLVIELEDLGPQBFELVAYWR 171
DB	340	NEIGPPDVKVDISDVLH-----IKITPPG-----GPGNKIMSDLYD----PSYQILYWK 385
QY	172	REPGEAEHVKNVRSGGIPVHLETMPEGAAYCVKAQTFVKAIGRYSAFSQTECV-EVQGEA 230
DB	386	NSDNEEEVKMKETKTOTIATVSDLAPESTLYCVKQVAFSEAYNKSSDFSREECIGTAGGKH 445
QY	231	IPLVLFALFAFVGMFLILVVPV-----LFVWMGRLLQYSCCPVVVLPDTL-----KITNSP 281
DB	446	LPILII-LATFAGALTAVLIVASLIVFLYQVYNKIKYMFPPSCQTPNIEGFGAQLFSSP 504
QY	282	QKLISCRREEVDAC 295
DB	505	--FVPTVERPVEIC 516
RESULT 5		
Q5XP11 CHICK PRELIMINARY; PRT; 569 AA.		
AC	Q5XP11	
DT	25-OCT-2004 (T-EMBLrel. 28, Created)	
DT	25-OCT-2004 (T-EMBLrel. 28, Last sequence update)	
DT	25-OCT-2004 (T-EMBLrel. 28, Last annotation update)	
DE	Interferon receptor.	
GN	Names=IFNAR1;	
OS	Gallus gallus (Chicken).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;	
OC	Gallus.	
OX	NCBI_TaxID=9031;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RC	TISSUE=Liver;	
RA	Han C.-L., Wang M., Gao F., Wu Z.-G.;	
RL	Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AY741159; AAU93528.1; -, mRNA.	
DR	GO; GO:0016020; C:membrane; IEA.	
DR	GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.	
DR	GO; GO:0004872; F:receptor activity; IEA.	
DR	InterPro; IPR000282; Cytok_receptor_2.	
DR	InterPro; IPR003961; FN_III.	
DR	SMART; SM00060; FN3; 3.	
DR	PROSITE; PS00853; FN3; 4.	
KW	Receptor.	
SQ	SEQUENCE 569 AA; AEC99111A5476FBF CRC64;	
Query Match		12.7%; Score 208; DB 2; Length 569;
Best Local Similarity		25.2%; Pred. No. 2.1e-09;
Matches		79; Conservative 52; Mismatches 125; Indels 58; Gaps 14;
QY	21	YALIPCL-LTDEVAIIPAPONLSVLSTNMKHLWSPVAPGTIVYVSVEY-OGEYESLY 78
DB	222	FSPHICIKTRKYNLDLCPNTNRVFPALNMKFFYLWDNHY--NSHVTYTVQVLTGYLKNLY 279
QY	79	T--SHWIPSSWCSLTEGPECDDVTDDITAT-VPYNLRVRATLGSQTSAMS-----125
DB	280	DYSSKQKVGCGENITSMKCNLSVVKPTASYYFRVQAMNEYKSLSKDVEVDPVPT 339
QY	126	-----ILKHPFNRRNSTILTRPGMBITKDGPHLVIELEDLGPQBFELVAYWR 171

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Viallao D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP PROTEIN SEQUENCE OF 20-34.
 RX PubMed=15340161; DOI=10.1110/ps.04582504;
 RA Zhang Z., Henzel W.J.;
 RA "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites.";
 RL Protein Sci. 13:2819-2824(2004).
 RN [7]
 RP CHARACTERIZATION.
 RX MEDLINE=97459974; PubMed=9312047; DOI=10.1093/emboj/16.19.5894;
 RA Kotenko S.V., Krause C.D., Izotova L.S., Pollack B.P., Wu W.,
 RA Pestka S.;
 RT Identification and functional characterization of a second chain of
 RT the interleukin-10 receptor complex.";
 RL EMBO J. 16:5894-5903(1997).
 RN [8]
 RP CHARACTERIZATION.
 RX MEDLINE=20469498; PubMed=10875937; DOI=10.1074/jbc.M005304200;
 RA Xie M.-H., Aggarwal S., Ho W.-H., Foster J., Zhang Z., Stinson J.,
 RA Wood W.I., Goddard A.D., Gurney A.L.;
 RT Interleukin (IL)-22, a novel human cytokine that signals through the
 RT interferon receptor-related proteins CRF2-4 and IL-22R.";
 RL J. Biol. Chem. 275:31335-31339(2000).
 CC -!- FUNCTION: Receptor for IL10 and IL22. Serves as an accessory chain
 CC essential for the active IL10 receptor complex and to initiate
 CC IL10-induced signal transduction events.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the type II cytokine receptor family.
 CC -!- SIMILARITY: Contains 2 fibronectin type-III domains.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; Z17227; CAA78933.1; -; mRNA.
 DR EMBL; U08988; AAA86872.1; -; Genomic DNA.
 DR EMBL; BT009777; AAP88779.1; -; mRNA.
 DR EMBL; AV323826; AAP72016.1; -; Genomic DNA.
 DR EMBL; BC001903; A3H01903.1; -; mRNA.
 DR F1R; A47003; A47003.
 DR HSSP; P13726; 1TFH.
 DR ENSEMBL; ENSG00000159113; Homo sapiens.
 DR HGNC; HGNC:5965; IL10RB.
 DR H-InvDB; HIX0016074; -.
 DR MIM; 123889; -; C:integral to membrane; TAS.
 DR GO; GO:0016021; -; C:integral to membrane; TAS.
 DR GO; GO:0005886; C:plasma membrane; TAS.
 DR GO; GO:0004920; F:interleukin-10 receptor activity; TAS.
 DR GO; GO:0004872; F:receptor activity; TAS.
 DR GO; GO:0006954; P:inflammatory response; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR000282; Cytok receptor 2.
 DR InterPro; IPR003961; FN III.
 DR Pfam; PF01108; Tissue fac; I.
 DR PROSITE; PS00853; FN3_FALSE_NEG.
 KW Direct protein sequencing; Glycoprotein; Polymorphism; Receptor;
 KW Signal; Transmembrane.

FT SIGNAL 1 19 Interleukin-10 receptor beta chain.
 FT CHAIN 20 325 Extracellular (Potential).
 FT TOPO_DOM 20 220 Potential.
 FT TRANSMEM 221 242 Potential.
 FT TOPO_DOM 243 325 Cytoplasmic (Potential).
 FT DOMAIN 113 205 Fibronectin type-III.
 FT CARBOHYD 49 49 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 68 68 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 102 102 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 161 161 N-linked (GlcNAc...) (Potential).
 FT DISULFID 66 74 By similarity.
 FT DISULFID 188 209 By similarity.
 FT VARIANT 47 47 K -> E (in dbSNP:2834167).
 FT FTID=VAR 020666.
 FT CONFLICT 124 124 A -> D (in Ref. 2).
 FT CONFLICT 243 243 A -> S (in Ref. 1 and 2).
 FT CONFLICT 269 273 FLAGHP -> VGRME (in Ref. 2).
 FT CONFLICT 274 325 Missing (in Ref. 2).
 SQ SEQUENCE 325 AA; 36995 MW; E470726619AF54C2 CRC64;
 Query Match 12.4%; Score 204; DB 1; Length 325;
 Best Local Similarity 27.1%; Pred. No. 2.5e-09;
 Matches 79; Conservative 47; Mismatches 113; Indels 52; Gaps 17;
 QY 12 WTSLEWFFVYALPCLLTDEVAIPAPONLSVLSTNMKHLMM-SPIVAPGETVYVSVEY 70
 Db 3 W-SLGSW-----LGGCLLVSAIGALGVPPPPVNVNFKILQWESPAFAKG-----NLTF 52
 QY 71 QGEYESLYTSHIWPSWCSLTGEPEDVTDITATVPYNLRVRLATLGQTSAM-SILKH 129
 Db 53 TAYLSYR-----IFQDKCMNTTLTECDFS-SLSKYGDHTLRVRAEFADSHSDWNITFC 106
 QY 130 PNRNSTILTRQPM--EITKDGPHLVIELEDLGPQE-----FLVAYWR 171
 Db 107 PV--DDTIIGPGQMQLVLAADSLH-----MRLAPKIENEYETWTKNVNWSWTYNVQYWK 160
 QY 172 REPGAEEHKVVRSGGIPVHLEMTBPGAAVCVKAQTFVKAIGRYSAFQSOTECVE-VQGEA 230
 Db 161 N--GTDEKQITFPQYDFEV-LRNLEPWYTCVQVRGFLDRNKAGWSEPVCEQTHDET 217
 QY 231 IP---LVLAFAFVGFMLILVVVPLF--VWKMGRLLQYSCCPVVVLPDTLK 276
 Db 218 VFSMVAVILMASV-FMVCLALLGCFALLWCYVVKTKYAFSPRNSLPQHLK 267
 RESULT 7
 Q5RL90 CHICK
 ID Q5RL90 CHICK PRELIMINARY; PRT; 334 AA.
 AC Q5RL90
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE IFNGR2 (interferon-gamma receptor 2).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RA Han C.-L., Wang M., Gao F., Wu Z.-G.;
 RL Submitted (Nov-2004) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RA Han C.-L., Wang M., Gao F.;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY820753; AAV67776.1; -; mRNA.
 DR EMBL; AY957508; AAX83125.1; -; mRNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain...); IEA.

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DR GO: GO:0007596; P: blood coagulation; IEA.
DR InterPro: IPR000282; Cytochrome c_2.
DR InterPro: IPR003961; FN III.
DR InterPro: IPR001187; Tissue factor.
DR Pfam: PF01108; Tissue_fac_1.
DR PROSITE: PS0853; FN3; 2.
KW Receptor.
SQ SEQUENCE 334 AA; 37698 MW; 5951976B878FC1F6 CRC64;
  Query Match 12.1%; Score 199.5; DB 2; Length 334;
  Best Local Similarity 24.7%; Pred. No. 6.3e-09;
  Matches 79; Conservative 58; Mismatches 130; Indels 53; Gaps 17;
QY 15 LFMWFFYALIPCLL--TDEVAIPAPQNLVSLSTNMKHLMMSPVIAPGETVYYSVEYQ- 71
Db 8 LFLVIGIFLLGPARAPGTEASPHLPAPEDVMVYSFNFCSNLSRSPVKVDGSGSVYTVQFKT 67
QY 72 GEYESLYSHWIIPSW-----CSLTGREGPCDVDDITATVPYNLVRATILGTSOTSAW 124
Db 68 GAF-----NHWSEMDCTRIQTGCSFLKSVKERRWTVV--LRVRAEMGPRTSAW 114
QY 125 SILKHPPF--NRNSTI--LTRPGMEITKDGPHLVIELEDLGPQ-----PEFLVAYMRREPAGAE 177
Db 115 -VETDFVAERNNTTIGPPKNSVIVSSDLLISVTPFPFGPEPGYHLQYHVSYWENTTITT 173
QY 178 EHVQMVRSGGIPVHLETMPGAAVCVKAQTFVKAIGRYSAFS-QT--ECVEV---OGEAI 231
Db 174 K--KEIKTSNTLPKINDKQSLTYCTFIQIELMTYSRFLHGLQTVPCYVRTTISEATKA 231
QY 232 PLVLALFAPVGMFLILVVVPLF--VWKMGRLLQYSCCPVVVLP-----DTLKINSPOKLIS 286
Db 232 GVTVAIFMSVGLLIIIVIGFFCLWRNKAIKYLSQPLRIPSHFPEYLRDPSPMPOLEVL 291
QY 287 CRREEVDACATVMSPEELL 306
Db 292 ENHDE-----DPQDL 302
RESULT 8
Q6ZVU9 HUMAN
ID Q6ZVU9_HUMAN PRELIMINARY; PRT; 327 AA.
AC Q6ZVU9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ42063.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Synovial membrane tissue;
RA Suzuki O., Sasaki N., Aotsuka S., Shoji T., Ichihara T., Shiohata N.,
RA Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y.,
RA Matsumura Y., Moriya S., Chiba E., Moniyama H., Onogawa S.,
RA Kaeriyama S., Satoh N., Matsunawa H., Takahashi E., Kataoka R.,
RA Kuga N., Kuroda A., Satoh I., Kamata K., Takami S., Terashima Y.,
RA Watanabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A.,
RA Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
RA Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K.,
RA Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.,
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
DR EMBL; AK124057; mRNA.
DR GO: GO:0016020; C-membrane; IEA.
DR GO: GO:0004896; F: hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO: GO:0004872; F: receptor activity; IEA.
DR InterPro: IPR000282; Cytochrome c_2.
KW Receptor; Transmembrane.
SQ SEQUENCE 327 AA; 37430 MW; DACB38F7312B0EF6 CRC64;
  Query Match 11.9%; Score 195.5; DB 2; Length 327;
  Best Local Similarity 26.4%; Pred. No. 1.4e-08;
  Matches 73; Conservative 48; Mismatches 109; Indels 47; Gaps 15;
QY 26 CLLTDEVAIPAPQNLVSLSTNMKHLMM--SPVIAPGETVYYSVEYQGYESLYTSHWI 84
Db 14 CLIFITAGLMVPPPPENVRMNSVNFKNILQWESPAFAG-----NLTFQAQVLSYR-----I 63
QY 85 PSWSCLSTGPEPCDVDDITATVPYNLVRATILGTSOTSAW--SILKHPFNNSILTRPGM 143
Db 64 FQDKCMNTTLTGECDFS--SLSKYGDHTLRVRAEFADSHSDWNITFCPV--DDTIIIGPPGM 120
QY 144 --EITKDGPHLVIELEDLGPQFE-----FLVAYMRREPAGAEHVKMVR 185
Db 121 QVEVLADSLH---MRFLAPKLENEYETWTKMKNVSNWTYNQYKWN--GTDEKFOITPQ 174
QY 186 GGIPIVHLETMPGAAVCVKAQTFVKAIGRYSAFSQTCEVE--VQGEAIP---LVLAALFAFV 241
Db 175 YDPEV--LRNLEPWTTCVQVRGFLPDRNKAGSEWSEPCQTTHDETVPSPMVAIVLASV 233
QY 242 GFMILILVVVPLF--VWKMGRLLQYSCCPVVVLPDTLK 276
Db 234 -FMVCLALGCFALLWCYVTKTKYAFSPRNSLPQHLK 269
RESULT 9
INARI_MOUSE
ID INARI_MOUSE STANDARD; PRT; 590 AA.
AC P33896;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC).
GN Name=ifnar1; Synonyms=Ifar, Ifnar;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92262522; PubMed=1533935;
RA Uze G., Lutfalla G., Bandu M.T., Proudhon D., Mogensen K.E.;
RT "Behavior of a cloned murine interferon alpha/beta receptor expressed
RT in homospesific or heterospesific background.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4774-4778(1992).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95047447; PubMed=7958966; DOI=10.1016/0378-1119(94)90710-2;
RA Lutfalla G., Uze G.;
RT "Structure of the murine interferon alpha/beta receptor-encoding gene:
RT high-frequency rearrangements in the interferon-resistant L1210 cell
RT line.";
RL Gene 148:343-346(1994).
CC -!- FUNCTION: Receptor for interferons alpha and beta. Binding to type
CC I IFNs triggers tyrosine phosphorylation of a number of proteins
CC including JAKs, Tyk2, STAT proteins and IFN alpha- and beta-
CC subunits themselves.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the type II cytokine receptor family.
CC -!- SIMILARITY: Contains 3 fibronectin type-III domains.
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CC use as long as its content is in no way modified and this statement is not
CC removed.
DR EMBL; M89641; AAA37890.1; -; mRNA.
DR F01; A45283; A45283.
DR Ensembl; ENSMUSG000000022967; Mus musculus.
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determined at the level of receptor (IFNAR) structure.";
RT FEBS Lett. 313:255-259(1992).
RN [2]
RX NUCLEOTIDE SEQUENCE.
RA MEDLINE=93305725; PubMed=8318540; DOI=10.1016/0167-4781(93)90129-2;
RL Lim J.-K., Langer J.A.;
RT "Cloning and characterization of a bovine alpha interferon receptor.";
RL Biochim Biophys. Acta 1173:314-319(1993).
CC -!- FUNCTION: Receptor for interferons alpha and beta. Binding to type
CC I IFNs triggers tyrosine phosphorylation of a number of proteins
CC including JAKs, TYK2, STAT proteins and IFN alpha- and beta-
CC subunits themselves.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the type II cytokine receptor family.
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CC removed.
CC -----
CC EMBL; X68443; CAA48484.1; -; mRNA.
DR EMBL; L06320; AAA02571.1; -; mRNA.
DR PIR; S27387; S27387.
DR InterPro; IPR000282; Cytok receptor_2.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR001187; Tissue factor.
DR Pfam; PF01108; Tissue fac; 1.
DR PROSITE; PS50853; FN3; 2.
KW Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 24 By similarity.
FT CHAIN 25 560 Interferon-alpha/beta receptor alpha
FT chain.
FT TOPO_DOM 25 437 Extracellular (Potential).
FT TRANSMEM 438 458 Potential.
FT TOPO_DOM 459 560 Cytoplasmic (Potential).
FT DOMAIN 133 224 Fibronectin type-III 1.
FT DOMAIN 230 326 Fibronectin type-III 2.
FT DOMAIN 334 426 Fibronectin type-III 3.
FT CARBOHYD 47 47 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 55 55 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 85 85 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 109 109 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 254 254 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 313 313 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 377 377 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 434 434 N-linked (GlcNAc...) (Potential).
FT DISULFID 76 84 By similarity.
FT DISULFID 199 220 By similarity.
FT CONFLICT 422 422 F -> V (in Ref. 2).
SQ SEQUENCE 560 AA; 63819 MW; 66D76B72861E1D11 CRC64;

Query Match 11.0%; Score 181.5; DB 1; Length 560;
Best Local Similarity 22.9%; Pred. No. 4.5e-07;
Matches 73; Conservative 62; Mismatches 133; Indels 51; Gaps 14;

QY 21 YALIPCLLTDEVAIPAPQNLVSLSTMKHLMMSPVIAGETVYVYVQGEYESLYTS 80
Db 215 YSPVYCINTERHKVSPENIQINADNQIYVLKW-----DYPENATFQAQLRAFFK 267

QY 81 HI-----W--IPSSWCSLITEGPECDDTDITATVPYNLRVRATLGSQTSAMSLKHPF 131
Db 268 KIPGNHSDKWQIPN--CENVSTHCVFPREVSSRGYYVVRVRSANGNGTSFWSSEKEFN 325

QY 132 NRRNSTLTLPGM---BITKDGPHLVI-----ELEDGPQ----PEFLVAYVRREPGEAEHV 180
Db 326 TEMKTIIFPPVISKSVTDLSHVSVCASESESNMNVNQIPLYEIVFWEINTSNAERKV 385

QY 181 KWRVSGGIPVHLETMEPGAAYCVKAQTFVKAIGRY--SAFSQTECVVEVQ----GEAIPLV 234
Db 386 LEKRTNFI---FPDLKPLTVYCVKARALIENDRRNKGSSFSFDVCEKTPGNTSKTWLIV 442

235 LALFAFVGFMLILVTVPLFWKMGRLLOYSCCPVVVLPDTLK--ITNSPOK--LISCRRE 290
443 GTCTALFSIPWYIYVVSVEL----RCVKYVFFPSPKPPSSVDYFSDQPLRNLSTSEE 498
291 EVDAC-----ATAVMSPEE 304
499 QTERCFIIENASIITEIEE 517

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Job time : 113.866 secs

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